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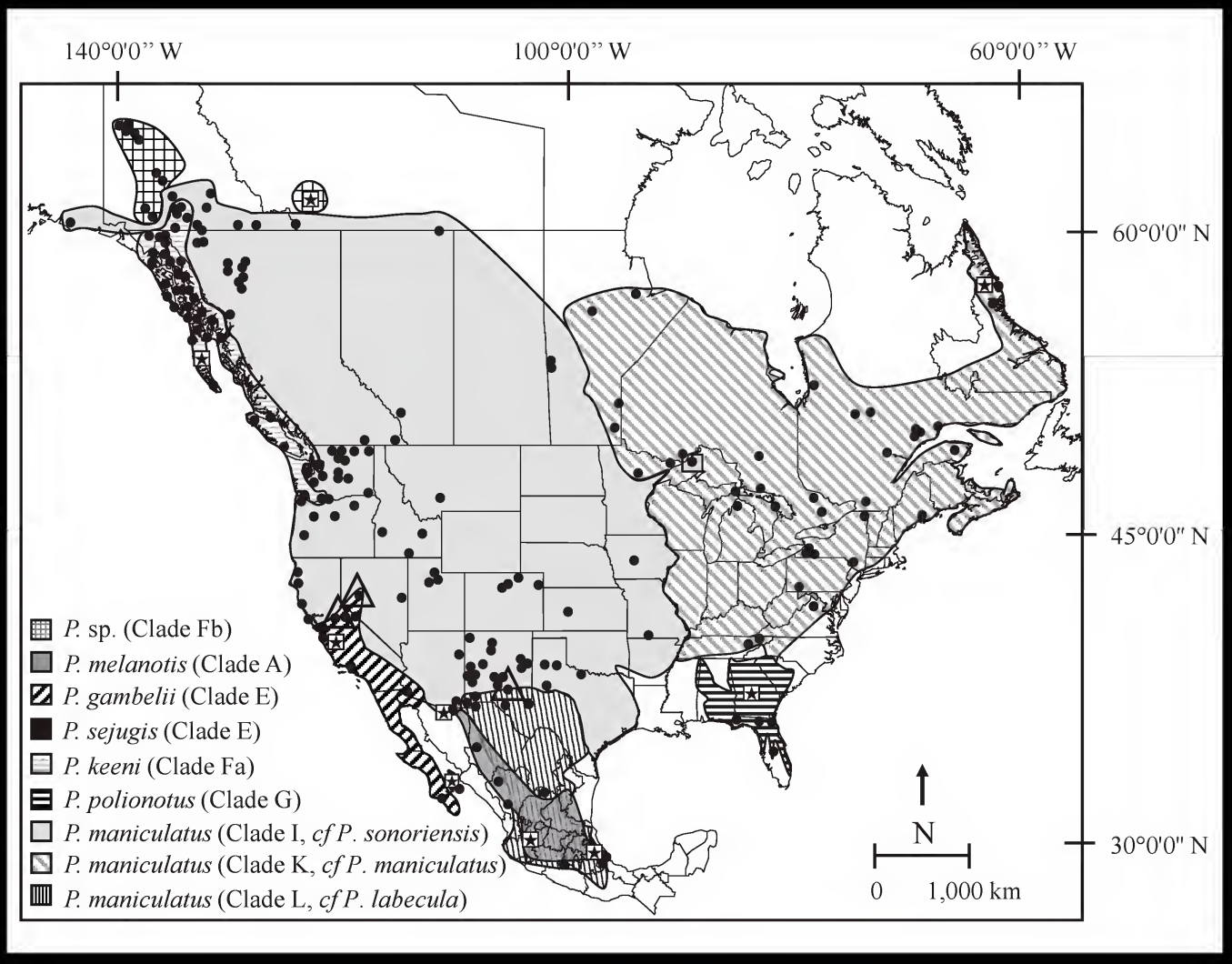
Mitochondrial DNA Sequence Data Indicate Evidence for Multiple Species Within *Peromyscus maniculatus*



Robert D. Bradley, James Q. Francis, Roy N. Platt II, Taylor J. Soniat, Daysi Alvarez, and Laramie L. Lindsey

Front cover: Distribution of selected populations and species of the *Peromyscus maniculatus* species group from Canada, Mexico, and the United States, as proposed herein. See Figure 1 for a more complete explanation. Figure by R. D. Bradley.

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Abstract

Peromyscus maniculatus is one of the most commonly encountered and intensively studied small mammal species in North America. Because of a broad geographic distribution (Canada to central Mexico), relatively large amounts of morphometric and genetic variation, and a voluminous taxonomic history, the taxonomic delimitations of this taxon have been difficult to discern. Herein, a comprehensive phylogenetic study was conducted to assess patterns of genetic variation throughout the range of *P. maniculatus* to resolve the taxonomy and ascertain the distribution of phylogroups. DNA sequences from the mitochondrial cytochrome-*b* gene were included from 681 individuals, representing 28 of the 68 recognized subspecies formally assigned to *P. maniculatus*, as well as all members assigned to the *P. maniculatus* species group, to assess genetic variation across a broad geographic context. Parsimony, Bayesian, and maximum likelihood analyses were conducted to determine phylogenetic relationships; further, genetic distances and divergence dates were approximated to assist in determining the time of origin for phylogroups. Results of these analyses reveal the presence of eight major phylogenetic groups. With one exception, each lineage appears to represent a unique phylogenetic group that corresponds to a distinct geographic region. Results are in agreement with other studies suggesting that *P. maniculatus* (*sensu lato*) contained multiple phylogroups. Recognition of phylogroups followed by the application of the principals of taxonomic priority indicate that: 1) samples from western Nevada, southern California, and Baja California should be referred to as *Peromyscus gambelii*; 2) samples from the southwestern Yukon should be referred to as *P.* sp.; 3) samples from southeastern Alaska and southcentral Yukon southward along coastal British Columbia to southwestern Washington should be referred to as *P. keeni*; 4) samples from central and western North America should be referred to as *Peromyscus sonoriensis*; 5) samples from eastern Canada and the eastern United States should be referred to as *P. maniculatus*; 6) samples from extreme southwestern New Mexico and central Mexico should be referred to as *Peromyscus labecula*; and 7) *Peromyscus sejugis* from Isla Santa Cruz, Baja del Sur, Mexico, should be tentatively retained as a valid species name. These seven species along with *Peromyscus melanotis* and *Peromyscus polionotus* comprise the *P. maniculatus* species group.

Key words: cryptic species, cytochrome-*b* gene, *Peromyscus maniculatus*, *P. maniculatus* species group, phylogenetics, systematics, taxonomy

Introduction

The North American Deermouse, *Peromyscus maniculatus* (Rodentia: Cricetidae), is a common rodent species distributed throughout most of North America (Hooper 1968), including the western and eastern portions of Canada, nearly all of the continental United States, and the central regions of Mexico.

Throughout its range, *P. maniculatus* inhabits a variety of habitats ranging from arid grasslands to mesic coniferous and hardwood forests. *Peromyscus maniculatus* has been considered as a cornerstone species in a variety of biological studies, including but not restricted to: biogeographical (Hanser and Huntly 2006), ecological (Taitt 1981; Kalkvik et al. 2012), chromosomal (Bowers et al. 1973; McAllister and Greenbaum 1997), population dynamics (Pulliam and Danielson 1991), natural variation (Bedford and Hoekstra 2015), behavioral (Hu and Hoekstra 2017), phylogeographic (Avise et al. 1987; Dragoo et al. 2006), reproductive (Fisher et al. 2016), insular biogeography (Foster 1963), coat coloration (Mallarino et al. 2017), and speciation (Bowers et al. 1973; Greenbaum et al. 1978). In addition, this species has been the focus for several studies of zoonotic diseases, including Hantavirus and Lyme (Schwan et al. 1989; Yates et al. 2002; Dragoo et al. 2006). Further, the *P. m. bairdii* genome recently was released (Worley 2015), thereby providing opportunities for future genetic studies.

Despite the voluminous number of studies centered on *P. maniculatus*, the taxonomy and systematics of *P. maniculatus* has been enigmatic and unresolved for many decades. For example, at least 68 subspecies have been described (Osgood 1909; Hooper 1968; Carleton 1989; Musser and Carleton 2005) as a result of morphologic diversity displayed across several diverse habitats, elevations, geography, and ecological niches (Osgood 1909; McCabe and Cowan 1945; Hall 1981; Carleton 1989; Musser and Carleton 2005).

Peromyscus maniculatus was described by Wagner (1845) based on specimens collected from the Moravian settlements in Labrador. In the years that followed Wagner's description, numerous species and subspecies were described (e.g. Merriam 1890; Rhoads 1894) as regions of the western United States and Canada were surveyed by mammalogists. In Osgood's (1909) revision of the genus *Peromyscus*, 35 subspecies of *P. maniculatus* were recognized and the *P. maniculatus* species group containing *P. maniculatus*, *P. melanotis*, *P. polionotus*, and *P. sitkensis* was established. Following Osgood's treatise, studies such as those by Nelson and Goldman (1931) and McCabe and Cowan (1945) contributed 22 additional subspecies to the taxonomy of this group.

Hooper (1968) provided a second revision of the genus and although he did not formally address subspecies, he indicated that 67 or 68 subspecies probably were represented under the *P. maniculatus* epithet. Further, Hooper (1968) assigned two species (*P. sejugis* and *P. slevini*) to the *P. maniculatus* species group. Later, Hall (1981) recognized 67 subspecies within *P. maniculatus* and maintained Hooper's vision of the *P. maniculatus* species group. Carleton (1989) followed Hooper's concept of the *P. maniculatus* species group but added *P. oreas* (based on chromosomal, allozymic, and morphologic data - Robbins and Baker 1981; Rogers et al. 1984; Gunn and Greenbaum 1986; Allard et al. 1987) as well as emphasizing that *P. oreas* and *P. m. austerus* were known to be sympatric in the Pacific Northwest. This elevation of *P. oreas* was short-lived as Hogan et al. (1993) reassigned *P. oreas* and *P. sitkensis*, along with 15 subspecies of *P. maniculatus* from the Pacific Northwest, to subspecific rank within *P. keeni.* The most recent classification (Musser and Carleton 2005) followed the position of Hogan et al. (1993) and treated *P. keeni* as a member of the *P. maniculatus* species group. In addition, several genetic studies (Hogan et al. 1997; Hafner et al. 2001; Dragoo et al. 2006; Walker et al. 2006) noted that samples of *P. keeni* and *P. sejugis* were more closely aligned with each other and to populations of *P. maniculatus* on Baja California, than to other populations of *P. maniculatus* from the western United States, suggesting that *P. maniculatus* in the western United States and Mexico may be paraphyletic relative to populations in the eastern United States. The case for including *P. slevini* in the *P. maniculatus* species group has been refuted by data presented in Hafner et al. (2001), who indicated that *P. slevini* should be considered as conspecific with *P. fraterculus* (assigned to the *P. eremicus* species group) and no longer associated with the *P. maniculatus* species group. Consequently, *P. slevini* will not be considered further in this study.

In a response to the importance of *P. maniculatus* in disease ecology (Lyme disease and Hantavirus), Dragoo et al. (2006) evaluated phylogeographic relationships among samples of *P. maniculatus* primarily from the northeastern and southwestern United States. These authors identified six genetic clades that loosely corresponded to the following geographic regions: Rocky Mountain states; Plains states; Pacific coast;

southwestern New Mexico and Mexico; northeastern United States and eastern Canada; and northeastern and northcentral United States and southcentral Canada. Further, Dragoo et al. (2006) confirmed that *P. maniculatus* is paraphyletic as currently recognized. Although they refrained from proposing taxonomic changes, they clearly identified the need for a major taxonomic re-appraisal. Later, studies by Gering et al. (2009), Kalkvik et al. (2012), and Sawyer et al. (2017) supported the general phylogenetic implications depicted in Dragoo et al. (2006), suggesting that distinct phylogenetic lineages occupy significantly different geographic regions.

Results of Wike's (1998) DNA sequence study involving populations of *P. maniculatus*- and *P. keeni*-like forms from the central Yukon, northern British Columbia, and southeastern Alaska indicated the presence of a third lineage apparently not affiliated with either *P. maniculatus* or *P. keeni*. This unpublished report remained largely ignored until Lucid and Cook (2007) and Sawyer et al. (2017) examined additional material and confirmed Wike's (1998) suspicions of an unassigned taxon in the southwestern Yukon. Wike (1998) discussed the possibility that "*arcticus*" (Mearns 1890), a name applied to populations in northwestern Canada, was available for this unassigned taxon (treated as *P. m. arcticus*, see Osgood 1904, 1909 but later subsumed into *P. m. borealis* by Mearns 1911). Although determining the correct name for this unassigned taxon is not a straightforward decision (discussed later in this treatise), it is clear that populations of *P. maniculatus* from the southwestern Yukon should be regarded as a species distinct from *P. maniculatus* and *P. keeni*. Consequently, for the remainder of this manuscript, *Peromyscus* sp. is used in reference to this unassigned taxon.

Recently, Greenbaum et al. (2017) used DNA sequence data obtained from mitochondrial genes (ND3-ND4L-ND4 region) to examine phylogenetic relationships within the *maniculatus* species group from western North America. Their study focused primarily on six subspecies of *P. maniculatus* from California, Oregon, and Washington, as well as samples of *P. keeni* and *P. sejugis*. Their results indicated that populations from southern California and Baja California (formerly assigned to *P. m. coolidegi* and *P. m. gambelii*) should be elevated to *Peromyscus gambelii*. Based on the limited sampling (Greenbaum et al. 2017), the geographic range of *P. gambelii* appears to extend from the northern boundary of the San Francisco Bay and the Sacramento and San Joaquin River drainages eastward into the Sierra Nevada Mountains and southward into Baja California.

Given the relatively large degree of morphological, chromosomal, and DNA sequence divergence identified in previous studies (discussed above) and especially the recent findings of Dragoo et al. (2006), Lucid and Cook (2007), Greenbaum et al. (2017), and others, it is apparent that *P. maniculatus* contains more than one phylogroup that may correspond to multiple undescribed species. Therefore, this study employs a broad-based taxonomic and geographic sampling scheme based on the synthesis of DNA sequences from the mitochondrial cytochrome-*b* (*Cyt*b) gene to: 1) estimate the magnitude of genetic variation within what currently is recognized as *P. maniculatus*; 2) determine the geographic distributions and phylogeographic patterns within *P. maniculatus* that could be useful in assessing taxonomic questions; 3) determine the phylogenetic relationships within the *P. maniculatus* species group; and 4) offer a taxonomic synthesis and approximate divergence dates for members of the *P. maniculatus* species group.

METHODS AND MATERIALS

Sampling.—Most DNA sequences used in this study were obtained from GenBank. To expand taxonomic and geographic coverage, 11 DNA sequences were obtained from tissue samples obtained from either naturally-occurring populations in Canada, United States, and Mexico or were borrowed from museum collections. See Figure 1 and the Appendix for a depiction of sampling sites and specimen information. An

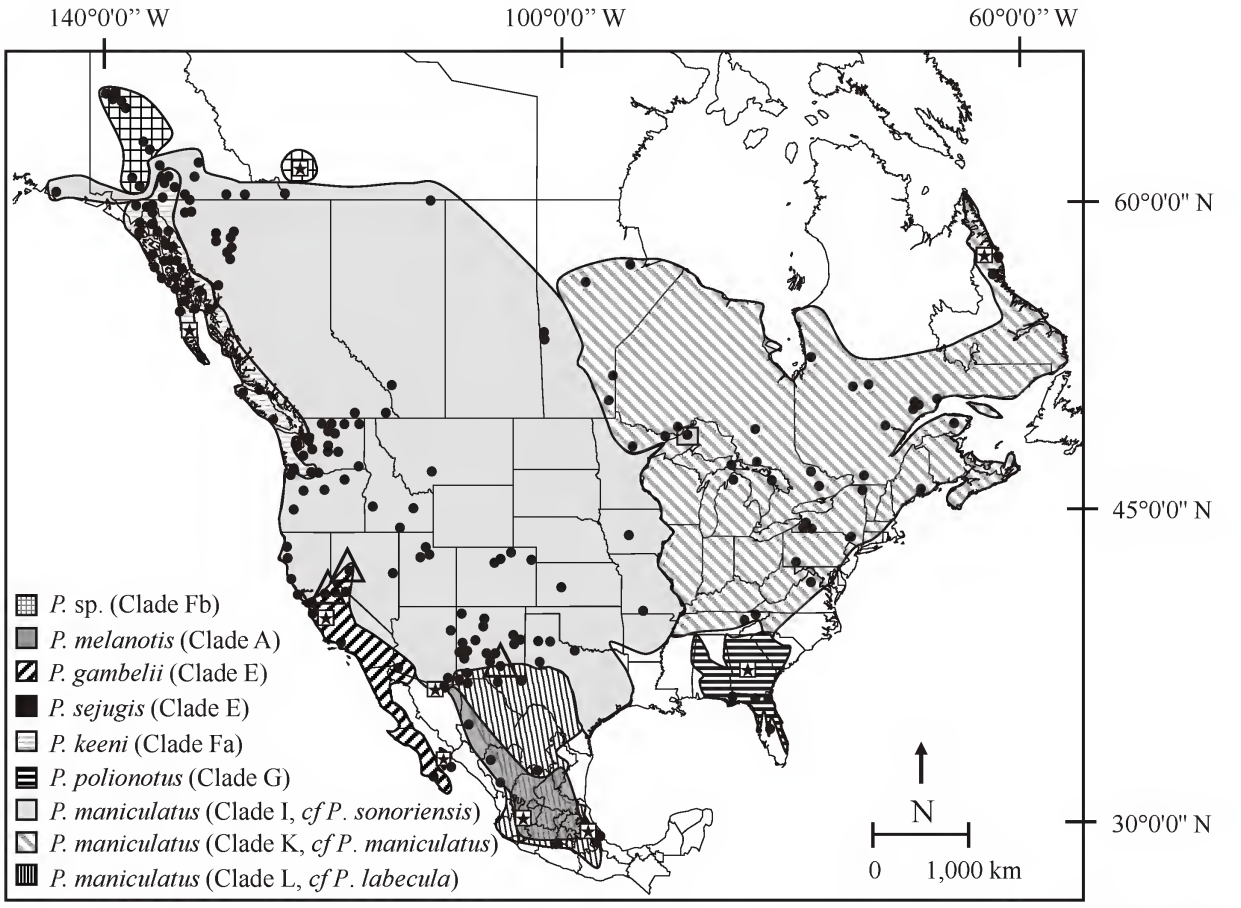

Figure 1. Distribution of selected populations and species of the *Peromyscus maniculatus* species group from Canada, Mexico, and the United States. Shaded areas represent distributions of taxa (defined in figure insert) as originally defined by Hall (1981) and modified based on the results of this study. Closed circles represent collecting localities listed in the Appendix; note that multiple individuals may be represented by a single closed circle. White boxes with black stars indicate type localities for each taxon and triangles indicate localities where haplotypes representing *P. sonoriensis* were found to be in sympatry with samples of *P. gambelii* and *P. labecula*, respectively.

attempt was made to include as many subspecies of *P. maniculatus* as possible (as recognized by Osgood 1909; Hall 1981; Musser and Carleton 2005) and the broadest geographic sampling that incorporated the genetic clades identified in previous studies (reported in Dragoo et al. 2006; Lucid and Cook 2007; Gering et al. 2009; Kalkvik et al. 2012; Greenbaum et al. 2017; Sawyer et al. 2017). Sequences of *P. melanotis*, *P. polionotus*, *P. keeni*, *P. sejugis*, and *P. gambelii* were included as internal reference taxa based on their status as members of the *P. maniculatus* species group, and sequences of *P. leucopus* and *P. gossypinus* were used as outgroups based on the phylogenetic information presented in Bradley et al. (2007) and Platt et al. (2015a).

All specimens collected for this study followed the methods outlined in the ASM Guidelines (Sikes et al. 2016) and protocols approved by the Texas Tech University Animal Care and Use Committee (protocol #17023-02).

DNA sequencing.—For the 11 additional specimens, mitochondrial DNA was extracted from frozen liver samples (0.1 g - obtained from wild caught rodents) following the standard protocol provided by the Qiagen DNeasy Blood and Tissues kit (Qiagen, Valencia, California). The complete *Cyt*b gene (1,143 base pair) was amplified using the polymerase chain reaction (PCR) method (Saiki et al. 1988) and the primers LGL

765 and LGL 766 (Bickham et al. 1995; Bickham et al. 2004). All reactions followed the standard HotStarTaq (Qiagen Inc., Valencia, California) protocol: 25-µL reactions containing 30 ng of DNA, 125 units of HotStart Taq premix, 10 µM of each primer, and 8.3 µL of distilled water (ddH_2O). The thermal profile was as follows: 80°C for Hotstart, 95°C for 2 minutes, followed by 34 cycles of 95°C for 30 seconds, 45°C for 45 seconds, and 73°C for 1 minute, with a final extension of 73°C for 10 minutes.

PCR products were purified using ExoSAP-IT (Affymetrix, Santa Clara, California). The following primers were used in cycle sequencing reactions to amplify fragments on the forward and reverse strands: 700H and 700L (Peppers and Bradley 2000; Tiemann-Boege et al. 2000) and either MVZ05 (Smith and Patton 1993) and MVZ14 (Smith 1998) or LGL 765 and LGL 766 (Bickham et al. 1995, 2004). Cycle sequencing reactions were purified using isopropanol cleanup protocols and were analyzed with an ABI 3100-Avant automated sequencer and ABI Prism Big Dye version 3.1 terminator technology (Applied Biosystems, Foster City, California). Resulting sequences were aligned using the software MUSCLE (Edgar 2004) and proofed using Sequencher 4.0 software (Gene Codes, Ann Arbor, Michigan) and chromatograms were proofed to verify all base changes. The 11 *Cyt*b sequences obtained in this study were deposited in GenBank and are listed in the Appendix.

Data analyses.—A neighbor-joining analysis (MEGA Version 6, Tamura et al. 2013) was conducted on an initial dataset containing 681 individuals: *P. gambelii*, n = 45; *P. keeni*, n = 179; *P. maniculatus*, n = 393; *P. melanotis*, n = 6; *P. polionotus*, n = 13; *P. sejugis*], n = 1; *P.* sp., n = 38; and outgroup samples (*P. leucopus*, n = 3 and *P. gossypinus*, n = 3) to verify taxonomic assignment, eliminate duplicate haplotypes, and confirm monophyly of clades. From this effort, the final dataset used in subsequent analyses included 501 individuals: *P. gambelii* (n = 41), *P. keeni* (n = 142), *P. maniculatus* (n = 265), *P. melanotis* (n = 5), *P. polionotus* (n = 13), *P. sejugis* (n = 1), *P.* sp. (n = 28), and the six outgroup sequences. Nearly all *Cyt*b sequences analyzed herein were complete sequences (1,143 bp) – fewer than 30 sequences were missing greater than 100 bp.

A parsimony analysis (PAUP* v. 4.0a165, Swofford 2002) was conducted using equally-weighted characters and variable nucleotide positions treated as unordered, discrete characters with four possible states; A, C, G, and T. Phylogenetically uninformative characters were removed from the analysis and the heuristic search and tree-bisection-reconnection option were used to estimate the most-parsimonious trees. A strict consensus tree was generated from the population of most-parsimonious trees and the bootstrap analysis of Felsenstein (1985) was used to evaluate nodal support (due to the computational requirements the "Fast Stepwise Addition" with 1,000 iterations was used).

Eighty-eight maximum likelihood models were evaluated using MODELTEST (Darriba et al. 2012), and the Akaike information criterion (AIC-Nylander 2004) identified the TIM3+I +G model of evolution (-lnL 12,586.6232) as being the most appropriate for the dataset. A likelihood analysis was performed using the program RAxML (Version 8.1.17, Stamatakis 2006) and the following parameters: base frequencies (A = 0.3596, C = 0.2704, G = 0.0988, and T = 0.2712), proportion of invariable sites (I = 0.3630), and gamma distribution (G = 0.6910) and the GTR+I +G because the RAxML program uses only the GTR model. Nodal support was evaluated using the bootstrap method (1,000 iterations, Felsenstein 1985), with bootstrap values (BS) $\geq$ 70 used to indicate moderate to strong nodal support.

A Bayesian analysis (MrBayes; Huelsenbeck and Ronquist 2001) was performed under a maximum likelihood framework to generate posterior probability values reflecting nodal support. The GTR+I+G substitution model and following options were used in this analysis: 4 Markov-chains, 10 million generations, and sampling every 1,000 generations. Inspection of the "stationary nature" of likelihood scores resulted in the first 1,000 trees being discarded and a consensus tree (50% majority rule) constructed from the remaining trees. Clade probability values (CPV; Huelsenbeck et al. 2002) $\geq$ 95 were used to reflect nodal support.

Genetic divergence and molecular dating.—Two methods were used to assess the magnitude of genetic differentiation and to approximate the timing of diver-

gence patterns. In the first method, the Kimura 2-parameter model of evolution (Kimura 1980) was used to estimate genetic distances among selected clades and taxa. These values were used to assess levels of genetic divergence relative to the genetic species concept following criteria outlined in Bradley and Baker (2001) and Baker and Bradley (2006). For example, several studies (Bradley et al. 2004, 2014, 2016, 2017) have shown that species of deermice generally differ by genetic divergence values ranging from 2 to 5%. These values could be used as a benchmark to evaluate whether level of genetic divergences within *P. maniculatus* (*sensu lato*) were indicative of multiple species. In the second method, a molecular clock test performed in MEGA (Version 6, Tamura et al. 2013), failed to reject a strict molecular clock. Divergence dates were estimated using BEAST v2.5.2 (Bouckaert et al. 2014). The maximum likelihood topology from RAxML was converted to an ultrametric tree with the ETE3 Python package and used as a starting tree (including branch lengths) in the BEAST analysis. For the remainder of the BEAST run, branch lengths were scaled but the topology was constrained to the ML tree. A prior log-normal distribution was placed on root height and used to constrain the divergence date estimates of the overall tree to ~1.5 MY with a σ value of 2. Calibrations used in the model were based on the fossil date between *P. gossypinus* and *P. leucopus* (Dalquest 1962; Karow et al. 1996) following methods outlined in previous studies (Bouckaert et al. 2014; Ordóñez-Garza et al. 2014; Platt et al. 2015a; Sullivan et al. 2017). Three test runs including the GTR+I+G model of evolution, 10,000,000 generations, and a 25% burn-in were used to optimize the analysis and to determine final parameters. Log and tree files were then combined to generate divergence date estimates and to produce a maximum clade credibility tree. The program Tracer (Bouckaert et al. 2014) was used to examine for sufficient mixing, convergence stability, and effective sample size >200 for all parameters, and TreeAnnotator (Bouckaert et al. 2014) was used to obtain an estimate of the phylogenetic tree.

RESULTS

Phylogenetic analyses.—Based on the results of the preliminary neighbor-joining analysis (n = 681), the dataset used for phylogenetic analyses (Bayesian, maximum likelihood, and parsimony) was pruned to (n = 501) 265 individuals of *P. maniculatus* (*sensu lato*) and 236 individuals representing outgroup and internal references samples. Topologies obtained from these three phylogenetic analyses were similar (congruent) in branching patterns located at the basal and mid-level nodes; most branching differences occurred at the terminal nodes where the exceptionally large number of taxa generated extraordinary possibilities for terminal associations. Consequently, the topology generated in the maximum likelihood analysis (Fig. 2A) was used to represent the phylogenetic relationships among samples examined herein. Support values obtained from each of the three analyses (CPV - Bayesian clade probability values, MLBS - maximum likelihood bootstrap, and PBS – parsimony bootstrap) were superimposed onto that tree (Fig. 2A). Basic tree descriptions and parameters obtained from the analyses are described below. For the parsimony analysis, a majority rule consensus tree was generated (not shown) from 9,530,901 equally most-parsimonious trees (length = 1,660, homoplasy index = 0.5908, and consistency index = 0.4092) that were available when the analysis was terminated due to computational constraints (tree storage issues). The large number of equally-parsimonious trees due to the extraordinarily high rearrangements at the tips of the tree produced as a result of numerous sequences differing by 1–2 bp. A tree score of -lnL 12,576.5390 was obtained from the maximum likelihood analysis.

Figure 2A depicts the topology and support values for each clade (A though M) identified across the three phylogenetic analyses; whereas, Figure 2B depicts the topology when unsupported clades (C, G, and H) were collapsed. Herein, Figure 2A is used to describe the composition and placement of the phylogenetic groups obtained from the three analyses. The five samples of *P. melanotis* (A; CPV = 1.00, MLBS = 100, and PBS = 100) formed a clade that was basal and sister to a clade (B; CPV = 0.98, MLBS = 35, and PBS = 52) containing samples of *P. gambelli*, *P. sejugis*, *P.* sp., *P. keeni*, *P. polionotis*, and *P. maniculatus* (*sensu lato*). Clade B was composed of two clades (C; CPV =

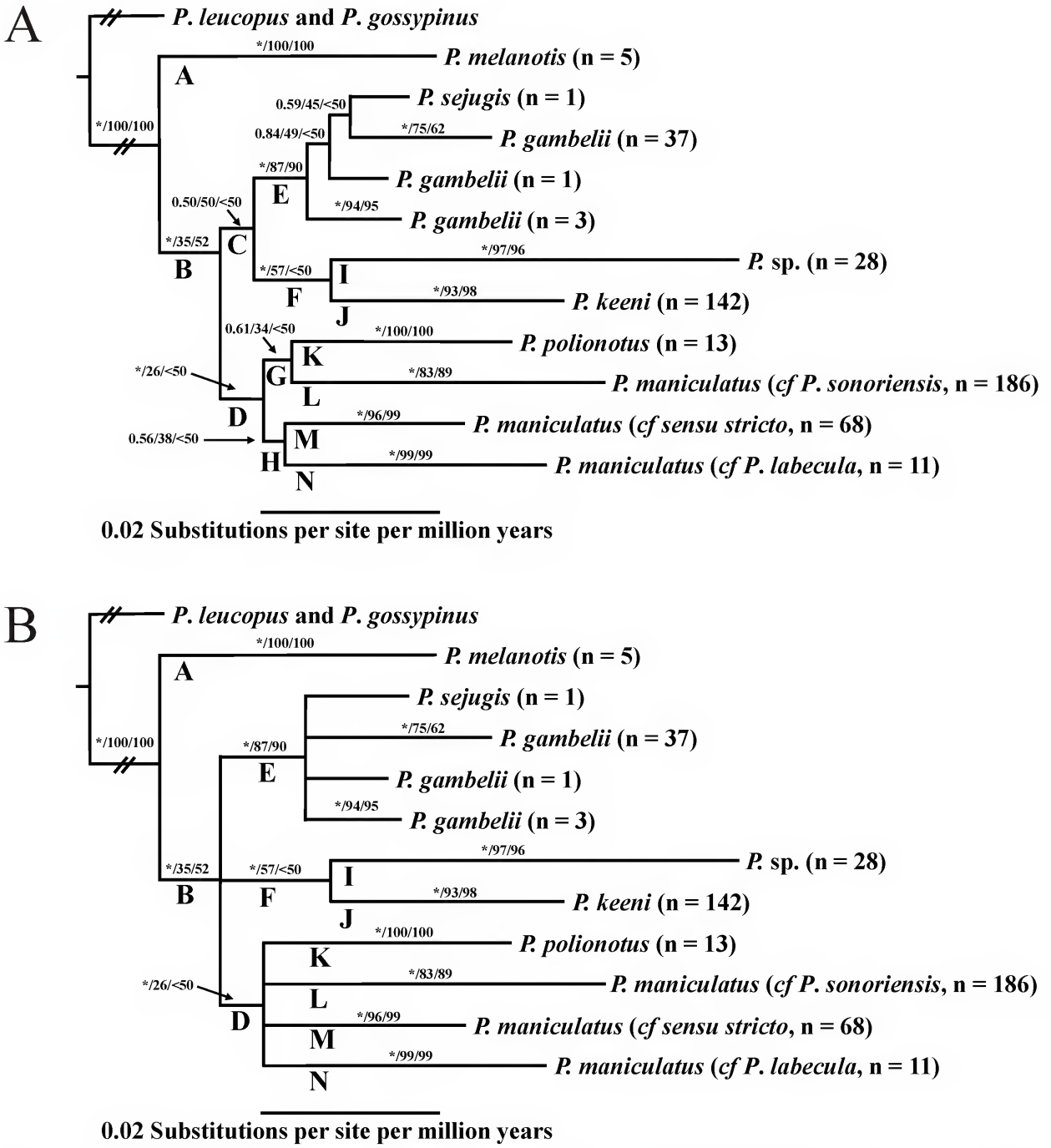

Figure 2. A) Phylogenetic tree generated using Bayesian (MrBayes; Huelsenbeck and Ronquist 2001), maximum likelihood (RAxML; Version 8.1.17, Stamatakis 2006), and parsimony methods (PAUP* v. 4.0a165, Swofford 2002) and DNA sequence data from the mitochondrial cytochrome-*b* gene. The topology depicted is from the Bayesian analysis. Clade probability values (≥ 0.95) for the Bayesian analysis are indicated by an asterisk (*) and are to the left of the first slash, bootstrap values for the maximum likelihood analysis are shown between the two slashes, and bootstrap values obtained from the parsimony analysis are to the right of the last slash. Line at bottom of figure depicts the nucleotide substitution rate per site per million years. B) Same phylogenetic tree as depicted in Figure 2A except unsupported nodes (C, G, and H) were collapsed.

0.50, MLBS = 50, and PBS = < 50 and D; CPV = 0.96, MLBS = 26, and PBS = < 50). Within clade C, two monophyletic clades were formed (E and F). Clade E (CPV = 1.00, MLBS = 87, and PBS = 90) contained the 41 individuals of *P. gambelii* and the single sample of *P. sejugis* and clade F (CPV = 1.00, MLBS = 57, and PBS = < 50) contained the 28 samples assigned to *P.* sp. (I; CPV = 1.00, MLBS = 97, and PBS = 96) and the 142 samples of *P. keeni* (J; CPV = 1.00, MLBS = 93, and PBS = 98). Clade D was comprised of two clades (G and H) with clade G (CPV = 0.61, MLBS = 34, and PBS = < 50) containing 13 samples identified as *P. polionotus* (K; CPV = 1.00, MLBS = 100, and PBS = 100) and 186 samples of *P. maniculatus* (L-*cf*, *P. sonoriensis*; CPV = 1.00, MLBS = 83, and PBS = 89) from the western portions of the United States and western Canada. Clade H (CPV = 0.56, MLBS = 38, and PBS = < 50) contained two clades (M and N) which were represented by 68 samples of *P. maniculatus* (M-*cf*, *P. maniculatus sensu stricto*; CPV = 1.00, MLBS = 96, and PBS = 99) from eastern Canada, Great Lakes region, and the eastern United States and 11 samples of *P. maniculatus* (N-*cf*, *P. labecula*; CPV = 1.00, MLBS = 99, and PBS = 99) from extreme southern United and northcentral Mexico.

Genetic distances.—Genetic distance values (Kimura 2-parameter, Table 1) were calculated to depict levels of genetic divergence between selected clades and taxa. Comparison of the magnitude of genetic divergence between species depicted values ranging from 2.05% (*P. gambelii* and *P. sejugis*) to 6.77% (*P. melanotis* and *P. polionotus*); whereas values estimated for comparisons within species ranged from 0.50% (*P. polionotus*) to 2.76% (*P. maniculatus sensu lato* - includes all remaining samples assignable to *P. maniculatus* as per Greenbaum et al. 2017). Genetic distances were then calculated within each of the three clades tentatively assignable to *P. maniculatus* by the phylogenetic analyses presented herein (L, M, and N; 1.27%, 1.69%, and 0.70%, respectively). These phylogroups were then compared to other currently recognized species in the *P. maniculatus* species group. For these comparisons, values ranged from 3.79% (Clade M and Clade N) and 3.80% (*P. gambelii* and Clade N) to 6.65% (*P. melanotis* and Clade M).

Table 1. Average genetic distances, estimated using the Kimura 2-parameter model of evolution (Kimura 1980), for selected comparisons of taxa within the *Peromyscus maniculatus* species group.

Samples evaluated	Genetic distance
Between species comparisons	
P. gambelii and *P. keeni*	3.71%
P. gambelii and *P. maniculatus* (*sensu lato*)	4.61%
P. gambelii and *P. melanotis*	5.31%
P. gambelii and *P. polionotus*	5.00%
P. gambelii and *P. sejugis*	2.05%
P. gambelii and *P.* sp.	5.00%
P. keeni and *P. maniculatus* (*sensu lato*)	5.15%
P. keeni and *P. melanotis*	6.19%
P. keeni and *P. polionotus*	5.20%
P. keeni and *P. sejugis*	3.97%
P. keeni and *P.* sp.	4.66%
P. maniculatus (*sensu lato*) and *P. melanotis*	6.18%
P. maniculatus (*sensu lato*) and *P. polionotus*	4.81%

Table 1. (cont.)

Samples evaluated	Genetic distance
P. maniculatus (*sensu lato*) and *P. sejugis*	4.71%
P. maniculatus (*sensu lato*) and *P.* sp.	4.67%
P. melanotis and *P. polionotus*	6.77%
P. melanotis and *P. sejugis*	4.80%
P. polionotus and *P. sejugis*	5.92%
P. sejugis and *P.* sp.	5.82%
Within species	
P. gambelii	0.98%
P. keeni	0.93%
P. maniculatus (*sensu lato*)	2.76%
P. melanotis	1.82%
P. polionotus	0.50%
P. sejugis	N/A
P. sp.	0.92%
Within clades of *P. maniculatus* (*sensu lato*)	
Clade L (*cf P. sonorensis*)	1.27%
Clade M (*cf P. maniculatus sensu stricto*)	1.69%
Clade N (*cf P. labecula*)	0.70%
Closely related clades in the *P. maniculatus* species group	
P. gambelii and Clade L (*cf P. sonorensis*)	4.55%
P. gambelii and Clade M (*cf P. maniculatus sensu stricto*)	4.90%
P. gambelii and Clade N (*cf P. labecula*)	3.80%
P. keeni and Clade L (*cf P. sonorensis*)	5.08%
P. keeni and Clade M (*cf P. maniculatus sensu stricto*)	5.34%
P. keeni and Clade N (*cf P. labecula*)	4.51%
P. melanotis and Clade L (*cf P. sonorensis*)	6.02%
P. melanotis and Clade M (*cf P. maniculatus sensu stricto*)	6.65%
P. melanotis and Clade N (*cf P. labecula*)	5.90%
P. polionotus and Clade L (*cf P. sonorensis*)	4.71%
P. polionotus and Clade M (*cf P. maniculatus sensu stricto*)	5.12%
P. polionotus and Clade N (*cf P. labecula*)	4.52%
P. sejugis and Clade L (*cf P. sonorensis*)	4.42%
P. sejugis and Clade M (*cf P. maniculatus sensu stricto*)	5.40%
P. sejugis and Clade N (*cf P. labecula*)	4.42%

Table 1. (cont.)

Samples evaluated	Genetic distance
P. sp. and Clade L (*cf P. sonorensis*)	4.80%
P. sp. and Clade M (*cf P. maniculatus sensu stricto*)	5.41%
P. sp. and Clade N (*cf P. labecula*)	4.60%
Clade L (*cf P. sonorensis*) and Clade M (*cf P. maniculatus sensu stricto*)	4.68%
Clade L (*cf P. sonorensis*) and Clade N (*cf P. labecula*)	4.28%
Clade M (*cf P. maniculatus sensu stricto*) and Clade N (*cf P. labecula*)	3.79%

Molecular dating.—A test of the molecular clock model (Tamura et al. 2013) indicated that the rates of genetic change were indicative of a strict molecular clock. The BEAST program estimated a Yule birth rate of 1.38 [(based on a 95% highest posterior density (HPD) that ranged from 0.89 to 1.72)]. The mean rate of evolution for *Cyt*b gene (depicted as substitutions per site per million years) was 0.94 (based on a 95% HPD) that ranged from 0.41 to 1.48). Divergence date estimates (Fig. 3) indicated that the initial split between the outgroup taxa (*P. gossypinus* and *P. leucopus*) and members of the *P. maniculatus* species group was 2.48 million years ago (mya). Divergence times associated with the origin of major clades ranged from 1.98 mya (*P. melanotis* from remaining species in the *P. maniculatus* species group) to 0.44 mya (*P. gambelii* and *P. sejugis*). The three clades containing samples historically assigned to *P. maniculatus* depicted divergences times of 1.40 mya (samples of *P. maniculatus* comprising Clade K and L) and 1.28 mya (samples of *P. maniculatus* comprising Clades M and N).

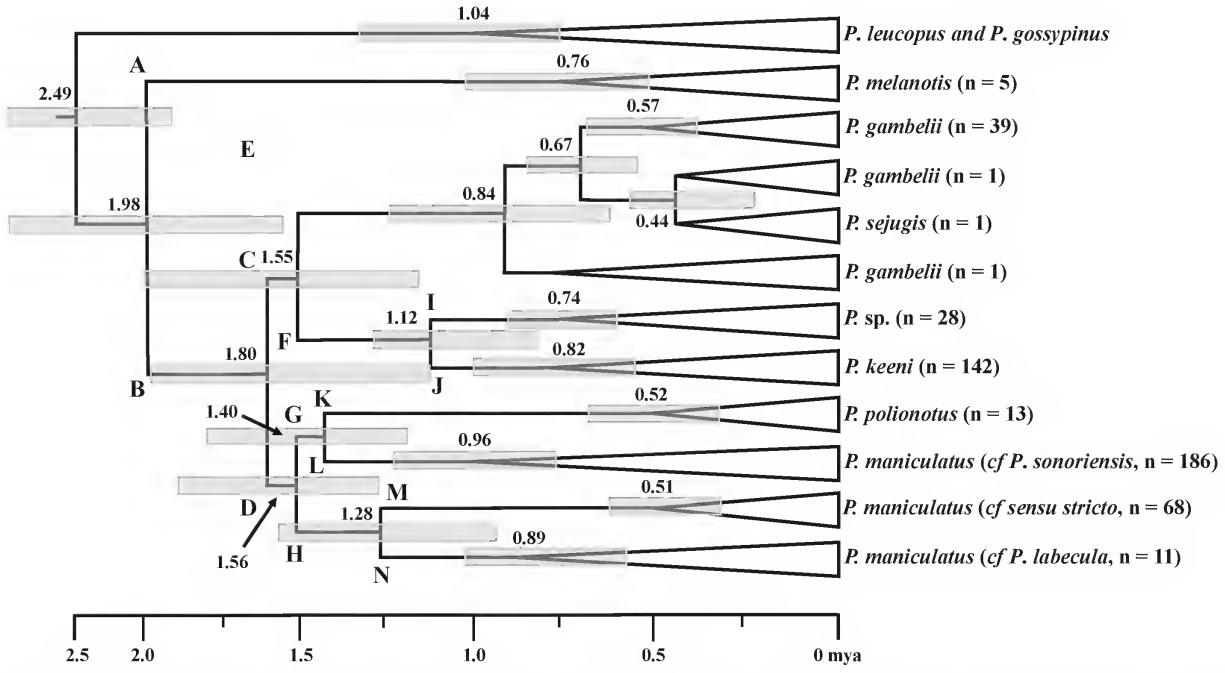

Figure 3. Time-calibrated ultrametric tree obtained from the BEAST analysis (Version 2.4, Bouckaert et al. 2014) of the mitochondrial cytochrome-*b* gene dataset. Scale bars at nodes represent the 95% highest posterior densities and numbers associated to each node are the estimated divergence times in million years ago.

DISCUSSION

Results of the parsimony, maximum likelihood, and Bayesian analyses of the *Cyt*b data indicated that *P. maniculatus*, as historically recognized, is represented by a complex of several distinct phylogeographic lineages. Given the strong association within each of the major phylogenetic clades (Clades E, I, K, L, M, and N; Fig. 2A), in respect to geographic ecoregions/habitats, it is probable that these phylogroups should be recognized as distinct species. One of these phylogeographic lineages (Clade E), *P. gambelii* (Baird 1857), was reinstated as a species by Greenbaum et al. (2017) based on evidence from chromosomes, morphology, DNA sequences, and microsatellites (Hooper 1944; Lansman et al. 1983; Hogan et al. 1997; Chirhart et al. 2005; Dragoo et al. 2006; Gering et al. 2009; Kalkvik et al. 2012; Sawyer et al. 2017). Similarly, *P.* sp. has been recognized as a species separate from *P. maniculatus* (Wike 1998; Lucid and Cook 2007; Sawyer et al. 2017) based on DNA sequences. However, three other phylogroups (Clades L, M, and N) appear to represent taxa (*cf P. labecula*, *P. maniculatus-sensu stricto*, and *P. sonoriensis*) that should be elevated to species status, the details and merits of which are discussed below. The significance of these lineages and the details associated with the taxonomic interpretation of these clades are discussed below.

Taxonomic Implications

Relative to taxonomic decision-making, there are several possible scenarios. Solutions to these various scenarios are based on interpretations of clade composition (branching patterns in the phylogeny), levels of nodal support (see below for more details), levels of genetic divergence between phylogenetic groups, resolution of paraphyly at a micro- or macroscale, acceptance of the currently recognized species: *P. melanotis*, *P. keeni*, *P. polionotus*, *P. gambelii*, *P. sejugis*, and *P.* sp. (perhaps assignable to *P. arcticus*) and taxonomic preference of lumping versus splitting.

The current dataset includes only mtDNA data and it is recognized that several studies (Wiens and Penkrot 2002; Carstens et al. 2013; Dool et al. 2016; Platt et al. 2018) object to implementing taxonomic decisions based solely on a mitochondrial marker. However, there have been a large number of studies conducted on *P. maniculatus* and its allies that have included a variety of systematic tools and data. Consequently, we have attempted to include support, from chromosomal, allozymic, morphologic, and other DNA sequence datasets in our final assessment. Further, because of the complexity of the species group, number of type localities that require sampling, and lack of contemporary tissue samples, no previous study has seriously attempted an all-inclusive revision of *P. maniculatus* since Osgood (1909). Therefore, it seems that there are two solutions, either develop a taxonomic hypothesis based on the data available at a given point in time (e.g. the mtDNA data included in this study that is supplemented with and supported by other published datasets, especially the phylogenetic relationships depicted in (Hogan et al. 1993, 1997; Dragoo et al. 2006; Lucid and Cook 2007; Kalkvik et al. 2012; Greenbaum et al. 2017; Sawyer et al. 2017) or continue to wait until a "gold standard dataset" that provides resolution of all branching patterns becomes available for analysis. Presumably, the gold standard dataset would include multiple nuclear genes, representatives from all type specimens (including recognized subspecies) and type localities, as well as a robust geographic coverage. At present, a gold standard dataset is not available; consequently, it appears that the best-case pathway relative to promoting the greatest possible taxonomic resolution is to present the most comprehensive dataset yet assembled and allow it to serve as an original hypothesis for testing as additional data become available.

Several of the solutions presented in the taxonomic implications are fairly straightforward and are supported by multiple lines of evidence. For example, the recognition of *P. melanotis*, *P. keeni*, *P. polionotus*, *P. gambelii*, and *P.* sp. (perhaps assignable to *P. arcticus*; see Wike 1998) as species are supported, in many cases, by chromosomal, allozymic, genetic (DNA sequences and microsatellites), and morphological data (Bowers et al. 1973; Avise et al. 1983; Calhoun et al. 1988; Hogan et al. 1993, 1997; McAllister and Greenbaum 1997; Chirhart et al. 2005; Dragoo et al. 2006; Lucid and Cook 2007; Gering et al. 2009; Kalkvik et al. 2012; Greenbaum et al. 2017; Sawyer et al. 2017; this study). The status of *P. sejugis* is less clear cut and

warrants careful attention (see species account for *P. sejugis* below). Although, we were unable to evaluate representatives of all recognized subspecies (see Hall 1981) in our analyses, especially insular forms; consequently, a combination of phylogenetic relationships among samples (as indicated by previous studies) and the distributions depicted in Hall (1981) was used to tentatively assign unsampled subspecies to the appropriate species.

Finally, it is acknowledged that support for monophyletic groups (equivalent to species as discussed herein) was strong; however, support for between relationships among groups was very weak (see Figs. 2A and 2B). This results in the conundrum of whether to reduce many of the clades depicted in Fig. 2A into an unresolved polytomy (Fig. 2B) or assume that clades are independently evolving groups that radiated rapidly with few synapomorphies having evolved to unite them. At the crux of this philosophical dilemma is do we draw attention to the major phylogenetic groups that are supported by the data at hand, or do we abandon all discussion on the basis that the phylogenetic relationships between clades are not supported. We chose to discuss the unsupported branching patterns recovered in our analyses rather than to reduce the tree to a series of polytomies and abandon a broader discussion of relationships; in doing so we highlight the independent nature of the major lineages and allow the reader to use the support values to determine where support exists, or not. A comparison of Figs. 2A and 2B allow for an alternative visualization of the putative relationships. For example, Clade D which contained samples of *P. maniculatus* (*sensu lato*) and *P. polionotus* could be inferred to include one or four species based on the acceptance of support values and philosophical interpretations of the principles of cladistics and systematic principles. If one chooses to recognize a single species, then *P. polionotus* would be relegated to subspecific status within *P. maniculatus*. If four species are recognized within clade D, then *P. polionotus* would remain as a species and based on taxonomic priority: Clade L would become *Peromyscus sonoriensis*, Clade M would remain as the nominal representative for *P. maniculatus* (*sensu stricto*), and Clade N would be named *Peromyscus labecula*. If the latter option is preferred, then the *P. maniculatus* species group would be expanded to include nine species.

P. polionotus as a valid species has received support based on a variety of chromosomal, allozyme, and DNA sequence data (Te and Dawson 1971; Bowers et al. 1973; Greenbaum et al. 1978; Avise et al. 1979, 1983; Robbins and Baker 1984; Stangl and Baker 1984), and based on the data presented herein (phylogenetic relationships and magnitude of genetic differentiation) and in following the criteria outlined under the Genetic Species Concept (see Baker and Bradley 2006), as well as the need for accurately drawing attention to previously unknown examples of biological diversity, we chose to recognize three cryptic species in what historically has been considered to be *P. maniculatus*. It is worth noting that all three taxa proposed for elevation to species level (*P. labecula*, *P. maniculatus*, and *P. sonoriensis*) are as genetically divergent from each other as they are from other species in the *P. maniculatus* species group (Table 1), and all three taxa were sufficiently distinct (morphologically) to originally be described as species (Wagner 1845; Le Conte 1853; Elliot 1903). In fact, divergence values for pairwise comparisons of *P. labecula*, *P. maniculatus*, and *P. sonoriensis* exceed that obtained when comparing *P. gambelii*, *P. keeni*, and the *P.* sp. from the Yukon region (Table 1). Further, comparison of divergence values among species in the *P. maniculatus* species group are similar to that reported for members within the *P. boylii* (Bradley et al. 2004, 2014, 2017) and *P. mexicanus* (Bradley et al. 2016) species groups, respectively.

Perhaps the strongest evidence supporting the recognition of *P. labecula*, *P. maniculatus*, and *P. sonoriensis* as species stems from the fact that haplotypes representing *P. sonoriensis* were found to be in sympatry with samples of *P. gambelii* and *P. labecula*, respectively. First, samples genetically referable to *P. sonoriensis* in western Nevada (NAS Fallon Air Force Base) and at two separate localities in east-central California (one in Mono County and one in Tuolumne County) appear to be sympatric with samples of *P. gambelii*. Of five individuals captured at the NAS Fallon Air Force Base, one individual was referred to *P. gambelii*, whereas the other four samples, genetically were assigned to *P. sonoriensis*. DNA sequence data obtained from five specimens collected from Mono County, California indicated that four samples were referable to *P. gambelii* and one sample was referred

to *P. sonoriensis*; whereas 10 specimens collected in Tuolumne County locality (collected near upper Lyell Canyon, Yosemite National Park) contained eight samples associated with *P. gambelii* and two samples that were referable to *P. sonoriensis*. Second, three samples genetically referable to *P. sonoriensis* and one sample of *P. labecula* were found to be sympatric in southcentral New Mexico (6.2 mi NW of Timberon). The occurrence of these species in sympatry, or near sympatry, indicates that they appear to be behaving as biological species (Mayr 1942) as well as genetic species (see Bradley and Baker 2001; Baker and Bradley 2006).

The first lineage (clade L) included samples from the central (west of the Mississippi River) and western portions of the United States and Canada. As previously discussed, genetic divergence values for members associated with Clade L, compared to other clades and taxa in this study, exceeded those of most species-to-species comparisons. For example, the comparison of Clade L to Clade K was 4.71% and was similar to divergence values (3.71%, 5.00%, and 4.66%) observed between clades containing samples of *P. gambelii*, *P. keeni*, and the *P.* sp. from the Yukon, respectively. Although we were only able to examine sequence data from samples representing eight subspecies, the geographic region estimated from these samples (Fig. 1) would suggest the inclusion of an additional eight subspecies based on the information presented in Hall (1981). If members of Clade L are sufficiently distinct from the other clades containing samples currently assigned to *P. maniculatus* (M and N), as the genetic data imply, then members of Clade L (total of 16 subspecies; see Table 2) should be assigned to *Peromyscus sonoriensis* (Le Conte 1853), which has priority based on the International Code of Zoological Nomenclature (1999). Additional details supporting the recognition of this taxon are provided under the species account for this taxon.

The second clade (M) containing samples of *P. maniculatus* included samples occurring in the northeastern portions of the United States and eastern Canada. Levels of genetic divergence for members associated with clade M, compared to other clades and taxa in this study, exceeded that for most species-to-species comparisons observed in this study. Of the three monophyletic clades containing samples of *P. maniculatus* (*sensu lato*, Clades L, M, and N) identified in this study; Clade M compared to Clade L and Clade N exhibited the smallest pairwise genetic distances (4.68% and 3.79%), respectively. Although we were only able to obtain DNA sequence data from samples representing six subspecies, the geographic region estimated from inclusion of these samples (Fig.1) would have included an additional three subspecies based on the information presented in Hall (1981). If members of clade M (total of nine subspecies formerly assigned to *P. maniculatus*) are sufficiently distinct from the other clades containing samples of *P. maniculatus* (L and N), as the genetic data imply, then members of Clade M should be assigned to *Peromyscus maniculatus* (*sensu stricto*, Wagner (1845) which has priority based on the International Code of Zoological Nomenclature (1999). Additional details supporting the recognition of this taxon are provided under the species account for this taxon.

The third Clade (N) was comprised of samples that currently are recognized as three subspecies of *P. maniculatus* (*blandus*, *fulvus*, and *labecula*). These samples occupy a broad geographic region (Fig. 1) in central and southeastern Mexico (Chihuahua, Durango, and Zacatecas then eastward to Veracruz) and an extreme southern portion of the United States (southern edge of New Mexico). Genetic divergence associated with members of this clade, relative to the other clades containing samples that formerly were recognized as *P. maniculatus* (Clades L and M), exceeded values obtained from other comparisons within the *P. maniculatus* species group except those involving pair-wise comparison with *P. melanotis*. For example, comparisons of Clade N to Clades K, L, and M revealed genetic distances of 4.52%, 4.28%, and 3.79%. Whereas, a comparison of *P. melanotis* to *P. keeni*, *P. maniculatus* (*sensu lato*), and *P. polionotus* produced genetic distances of 6.19%, 6.18%, and 6.77%, respectively. If members of clade N (*blandus*, *fulvus*, and *labecula*) are sufficiently distinct from members of the other clades (L and M) as the genetic data imply, then members of Clade N should be assigned to *P. labecula* (Elliot 1903) based on rules of priority as provided by the International Code of Zoological Nomenclature (1999). Additional details supporting the recognition of this taxon are provided under the species account for this taxon.

Table 2. Taxonomic assignments of subspecies as proposed from DNA sequence data generated herein and other published sources (Conroy and Cook 1999; Tiemann-Boege et al. 2000; Bradley et al. 2004, 2007; Arellano et al. 2005; Dragoo et al. 2006; Gering et al. 2009; MacDonald et al. 2009; Rodhouse et al. 2010; Kalkvik et al. 2012; Platt et al. 2015a; Sawyer et al. 2017). Type localities and authorities are presented for each subspecies. Yes or no indicates whether sequence data is available for a particular taxon. Letters in parentheses refer to clades depicted in Figure 2. An asterisk indicates the uncertainty of the type locality for *P.* sp.

Taxon	Type Locality	Authority	Sequence Data
P. sp. (Clade I)			
Monotypic	Fort Simpson, Yukon*	Mearns 1890	Yes
P. gambelii (Clade E)			
anacapae	Ventura Co., California	von Bloeker 1942	No
assimilis	Coronadas Island, Baja California Sur	Nelson and Goldman 1931	No
catalinae	Santa Catalina Island, California	Elliott 1903	No
cineritius	San Roque Island, Baja California	J. A. Allen 1898	No
clementis	Santa Barbara Islands, California	Mearns 1896	No
coolidgei	Santa Anita, Baja California	Thomas 1898	No
dorsalis	Natividad Island, Baja California	Nelson and Goldman 1931	No
dubius	Todos Santos island, Baja California	J. A. Allen 1898	No
elusus	Santa Barbara Island, Ventura, California	Nelson and Goldman 1931	No
exiguus	San Martin Island, Baja California	J. A. Allen 1898	No
exterus	San Nicolas Island, Santa Barbara Co., California	Nelson and Goldman 1931	No
gambelii	Los Angeles Co., California	(Baird 1857)	Yes
geronimensis	San Geronimo Island, Baja California	J. A. Allen 1898	No
hueyi	Gonzaga Bay, Baja California	Nelson and Goldman 1932	No
magdalenae	Magdalena Island, Baja California	Osgood 1909	No
margaritae	Margarita Island, Baja California	Osgood 1909	Yes
sanctaerosae	Santa Rosa Island, Santa Barbara Co., California	von Bloeker 1942	No
santacruzae	Santa Cruz Island, Santa Barbara Co., California	Nelson and Goldman 1931	No
streatori	San Miguel island, Santa Barbara Co., California	Nelson and Goldman 1931	No
P. keeni (Clade J)			
algidus	Bennett, British Columbia	Osgood 1909	Yes
angustus	Vancouver Island, British Columbia	Hall 1932	Yes
balaclavae	Balaclava Island, British Columbia	McCabe and Cowan 1945	No
beresfordi	Beresford Island, British Columbia	Guiguet 1955	No
cancrivorus	Queen Charlotte Sound, British Columbia	McCabe and Cowan 1945	No
carli	Cox Island, British Columbia	Guiguet 1955	No
doylei	Doyle Island, British Columbia	McCabe and Cowan 1945	No
georgiensis	Texada Island, British Columbia	Hall 1938	No
hylaeus	Prince of Wales Island, Alaska	Osgood 1908	Yes

Table 2. (cont.)

Taxon	Type Locality	Authority	Sequence Data
interdictus	Vancouver Island, British Columbia	Anderson 1932	Yes
isolatus	Vancouver Island, British Columbia	Cowan 1935	No
keeni	Graham Island, British Columbia	(Rhoads 1894)	Yes
macrorhinus	Skeena River, British Columbia	(Rhoads 1894)	Yes
maritimus	Moore Islands, British Columbia	McCabe and Cowan 1945	No
oceanicus	Forrester Island, Alaska	Cowan 1935	Yes
oreas	Whatcom Co., Washington	Bangs 1898b	Yes
pluvialis	Goose Island Group, British Columbia	McCabe and Cowan 1945	No
prevostensis	Queen Charlotte Sound, British Columbia	Osgood 1901	No
rubriventer	Hunter Islands, British Columbia	McCabe and Cowan 1945	No
sartinensis	Sartine Island, British Columbia	Guiguet 1955	No
sitkensis	Sitka, Alaska	Merriam 1897	Yes
triangularis	Triangle Island, British Columbia	Guiguet 1955	No
P. labecula (Clade N)			
blandus	Escalon, Chihuahua	Osgood 1904	Yes
fulvus	Oaxaca, Oaxaca	Osgood 1904	Yes
labecula	Ocotlan, Jalisco	Elliott 1903	Yes
P. maniculatus (Clade M)			
abietorium	James River, Nova Scotia	Bangs 1896	Yes
anticostiensis	Anticosti Island, Quebec	Moulthrop 1937	No
argentatus	Grand Manan Island, New Brunswick	Copeland and Church 1906	No
bairdi	McLean Co., Illinois	(Hoy and Kennicott 1857)	Yes
eremus	Magdaleen Islands, Quebec	Osgood 1909	No
gracilis	Madison Co., New York	(Le Conte 1855)	Yes
maniculatus	Moravian Settlements, Labrador	(Wagner 1845)	Yes
nubiterrae	Mitchell Co., North Carolina	Rhoads 1896	Yes
plumbeus	Saguenay Co., Quebec	C. F. Jackson 1939	Yes
P. melanotis (Clade A)			
Monotypic	Las Vigas, Veracruz	J. A. Allen and Chapman 1897	Yes
P. polionotus (Clade K)			
albifrons	Walton Co., Florida	Osgood 1909	No
allophrys	Walton Co., Florida	Bowen 1968	No
ammobates	Baldwin Co., Alabama	Bowen 1968	No
colemani	Spartanburg Co., South Carolina	Schwartz 1954	No
decoloratus	Volusia Co., Florida	A. H. Howell 1939	No
griseobracatus	Santa Rosa Co., Florida	Bowen 1968	No
leucocephalus	Okaloosa Co., Florida	A. H. Howell 1920	No
lucubrans	Allendale Co., South Carolina	Schwartz 1954	No
niveiventris	Brevard Co., Florida	(Chapman 1893)	No

Table 2. (cont.)

Taxon	Type Locality	Authority	Sequence Data
peninsularis	Bay Co., Florida	A. H. Howell 1939	No
phasma	St. Johns Co., Florida	Bangs 1898c	Yes
polionotus	somewhere in Georgia	Wagner 1843	No
rhoadsi	Hillsborough Co., Florida	Bangs 1898	Yes
subgriseus	St. Johns Co., Florida	(Chapman 1893)	Yes
sumneri	Bay Co., Florida	Bowen 1968	No
trissyllepsis	Baldwin Co., Florida	Bowen 1968	No
P. sejugis (Clade E)			
Monotypic	Santa Cruz Island, Baja del Sur	Burt 1932	Yes
P. sonoriensis (Clade L)			
alpinus	Revelstoke, British Columbia	Cowan 1937	No
artemisiae	Ashcroft, British Columbia	(Rhoads 1894)	Yes
austerus	Pierce Co., Washington	(Baird 1855)	Yes
borealis	Mackenzie, Northwest Territories	Mearns 1890 (may be *articus*)	Yes
hollisteri	San Juan Co., Washington	Osgood 1909	No
inclarus	Weber Co., Utah	Goldman 1939	No
luteus	Cherry Co., Nebraska	Osgood 1905	Yes
nebrascensis	Custer Co., Montana	(Coues 1877)	Yes
ozarkiarum	Washington Co., Arkansas	Black 1935	No
pallescens	Bexar Co., Texas	J. A. Allen 1896	Yes
rubidus	Mendocino Co., California	Osgood 1901a	Yes
rufinus	Coconino Co., Arizona	(Merriam 1890)	No
saturatus	Saturna Island, British Columbia	Bangs 1897	No
saxamans	Duncan Island, British Columbia	McCabe and Cowan 1945	No
serratus	Custer Co., Idaho	Davis 1939	No
sonoriensis	Santa Cruz, Sonora	(Le Conte 1853)	Yes

Peromyscus gambelii (Baird)

Hesperomys gambelii Baird, 1857:464.

Sitomys americanus thurberi J. A. Allen, 1893:185.

Peromyscus texanus clementis Mearns, 1896:4.

Peromyscus texanus medius Mearns, 1896:446.

Peromyscus leucopus coolidgei Thomas, 1898:145.

Peromyscus cineritius J. A. Allen, 1898:155.

Peromyscus geronimensis J. A. Allen, 1898:156.

Peromyscus exiguus J. A. Allen, 1898:157.

Peromyscus dubius J. A. Allen, 1898:157.

Peromyscus catalinae Elliot, 1903:10.

Peromyscus maniculatus gambelii Osgood, 1909:67.

Peromyscus maniculatus coolidgei Osgood, 1909:94.

Peromyscus maniculatus margaritae Osgood, 1909:95.

Peromyscus maniculatus clementis Osgood, 1909:96.

Peromyscus maniculatus catalinae Osgood, 1909:97.

Peromyscus maniculatus dubius Osgood, 1909:98.

Peromyscus maniculatus geronimensis Osgood, 1909:99.

Peromyscus maniculatus cineritius Osgood, 1909:100.

Peromyscus maniculatus magdalenae Osgood, 1909:101.

Peromyscus imperfectus Dice, 1925:123.

Peromyscus maniculatus assimilis Nelson and Goldman, 1931:305.

Peromyscus maniculatus streatori Nelson and Goldman, 1931:531.

Peromyscus maniculatus santacruzae Nelson and Goldman, 1931:532.

Peromyscus maniculatus exterus Nelson and Goldman, 1931:532.

Peromyscus maniculatus elusus Nelson and Goldman, 1931:533.

Peromyscus maniculatus martinensis Nelson and Goldman, 1931:534.

Peromyscus maniculatus dorsalis Nelson and Goldman, 1931:535.

Peromyscus maniculatus hueyi Nelson and Goldman, 1932:51.

Peromyscus maniculatus sanctaerosae von Bloeker, 1940:173.

Peromyscus maniculatus anacapae von Bloeker, 1942:161.

Peromyscus maniculatus exiguus Miller and Kellogg, 1955:485.

Holotype.—Osgood (1909) determined that an individual type was not dedicated by Baird (1857), however, one of Baird's original specimens (catalog number 369 deposited in the United States National Museum) was designated by Allen (1893) as the type for *P. gambelii*. This specimen was an adult; however, the specimen was reported to be in poor condition and the sex was unreported.

Type locality.—United States: California; Monterey.

Subspecies.—Includes *P. g. coolidgei* and *P. g. gambelii* based on the findings of Greenbaum et al. (2017), as well as *P. m. margaritae* according to the phylogenetic relationships of samples examined herein. Although we were not able to examine many of the subspecies that potentially are referable to *P. gambelii*, we tentatively assign the following 15 subspecies recognized by Hall (1981) to *P. gambelii*: *anacapae*, *assimilis*, *catalinae*, *cineritius*, *clementis*, *coolidgei*, *dorsalis*, *dubius*, *elusus*, *exiguous*, *exterus*, *gambelii*, *geronimensis*, *hueyi*, *magdalenae*, *margaritae*, *sanctaerosae*, *santacruzae*, and *streatori*.

Diagnosis.—Sides and upperparts ochraceous or ochraceous buff mixed with dusky coloration; underparts white; ears dusky; tail short to medium in length and bicolored (brown to dusky on top and white below). Medium sized for species group but possessing a longer than normal tail; measurements obtained from Osgood (1909), for several of the subspecies now assigned to *P. gambelii*, indicated a total length averaging 171.5 mm; (range 148–195 mm) and tail length averaging 84.5 mm (range 64–105 mm). Skull slightly smaller than that found in nearby populations of *P. maniculatus* and *P. sejugis* (Burt 1932).

Genetically (mitochondrial sequences; Hogan et al. 1997; Walker et al. 2006; Greenbaum et al. 2017; this study), *P. gambelii* has been shown to differ from other populations from the northwestern and western United States, formerly assigned to *P. maniculatus* but based on results presented herein (see Table 2) have been assigned to *P. sonoriensis* as well as other regional members of the *P. maniculatus* species group now assigned to *P. keeni*. In this study, data from the *Cyt*b analysis indicated that *P. gambelii* differed from *P. keeni*, *P. labecula*, *P. maniculatus*, *P. sonoriensis*, and *P. sejugis* by 3.71%, 3.80%, 4.90%, 4.55%, and 2.05%, respectively. Genetic differentiation (= 0.98%) based on DNA sequences obtained from 41 individuals of *P. gambelii* was among the lowest intraspecific values obtained in this study.

Distribution.—Based on data presented herein and from Greenbaum et al. (2017), the distribution of *P. gambelii* should include northern California (San Francisco Bay Area and San Joaquin Valley) and extreme western-central region of Nevada (west of the Sierra Nevada range), southward along coastal California to the southern tip of Baja California del Sur, Mexico. Further, it appears that samples from the northern portion of the former distribution of *P. m. gambelii* (as depicted by Hall 1981), specifically those from central Oregon and east-central Washington, should be assigned to *P. sonoriensis*. Although we were not able to examine many of the insular subspecies occurring along the California and Baja California coasts, presumably based on geographic location, those subspecies would be assignable to *P. gambelii*.

Comparison.—A member of the *P. maniculatus* species group. Similar in most characteristics to other members of the *P. maniculatus* species group; although smaller in size compared to *P. keeni* and *P. sonoriensis*. Hooper (1944) noted morphological distinctions between populations *P. gambelii* and populations north of the San Francisco Bay (now recognized as *P. sonoriensis rubidus*); with samples of *P. s. rubidus* averaging larger than *P. g. gambelii* in the following measurements: total length, tail length, length of braincase, length of nasals, and length of hindfoot. In addition, Hooper (1944) noted that samples referable to *P. s. rubidus* were darker and more reddish in color than were individuals referable to *P. gambelii*.

Remarks.—Forty-six samples were examined in this study that are assignable to *P. gambelii*. Of these samples, the closest to the type locality, examined herein, was approximately 50 km northeast of Monterey, California, United States.

Chromosomal variation within *P. gambelii* is extensive as the number of autosomal arms (fundamental number, FN) ranges from 72–86 (Bradshaw and Hsu 1972; Bowers et al. 1973; Calhoun et al. 1988) with *P. g. cooledgii* being reported as monomorphic (FN = 76; Calhoun et al. 1988) and *P. g. gambelii* being polymorphic (FN = 72–86; Calhoun et al. 1988). The FNs reported for *P. gambelii* overlap those reported for *P. labecula*, *P. maniculatus*, and *P. sonoriensis*; but differ substantially from those observed for *P. melanotis* (FN = 62, Hsu and Arrighi 1968; Bowers et al. 1973), *P. polionotus* (FN = 69–71; Te and Dawson 1971), and *P. sejugis* (FN = 76; Smith et al. 2000).

Although karyotypic, allozymic, and mtDNA restriction fragment length polymorphism datasets (Lansman et al. 1983; Calhoun et al. 1988) could not distinguish among populations of *P. maniculatus* from California and Baja California (now referable to *P. g. coolidgei*, *P. g. gambelii*, *P. s. rubidus*, and *P. s. sonoriensis*), recent genetic studies (Hogan et al. 1997; Dragoo et al. 2006; Walker et al. 2006; Greenbaum et al. 2017) indicated that *P. g. coolidgei* and *P. g. gambelii*, ranging from central California to Baja California del Sur were species distinct from *P. s. rubidus*, and *P. s. sonoriensis*. In addition, *P. gambelii* presumably was more closely related to *P. sejugis* and *P. keeni* than to other populations of *P. maniculatus* from the western United States (Avise et al. 1979; Gunn and Greenbaum 1986; Smith et al. 2000; Greenbaum et al. 2017); although Hogan et al. (1997), Chirhart et al. (2005), and this study posited that *P. sejugis* is sister to *P. keeni*. Although they did not include samples of *P. sejugis*, other studies (Dragoo et al. 2006; Kalkvik et al. 2012) demonstrated a close relationship between samples of *P. keeni* and *P. m. coolidgei* and postulated that coastal populations of *P. maniculatus* might represent a distinct genetic form. In addition, Kalkvik et al. (2012) reported that populations of *P. maniculatus* from southern California and Baja California (= *P. gambelii*) occupy significantly different climatic niches and ecozones than do populations of *P. maniculatus* from north of the San Francisco Bay (= *P. sonoriensis*). Herein, samples of *P. gambelii* exhibited extremely low genetic distance value with *P. sejugis* compared to other species examined. Estimated divergence times indicated that *P. gambelii* last shared a common ancestor with members of the *P. keeni/P. sp* clade approximately 1.55 mya. Further it appears that the *P. gambelii/P. sejugis/P. keeni* lineage diverged from other taxa formerly assigned to *P. maniculatus* (*P. labecula*, *P. maniculatus*, *P. polionotus*, and *P. sonoriensis* approximately 1.80 mya.

As discussed earlier, *P. gambelii* appears to be sympatric with samples of *P. sonoriensis* in western Nevada (near NAS Fallon Air Force Base) and at two separate localities in east-central California (one in Mono County and one in Tuolumne County). Additional data are need from these areas to determine if these genetic species (see Bradley and Baker 2001; Baker and Bradley 2006) are behaving as biological species (Mayr 1942) as well as genetic species.

Peromyscus keeni (Rhoads)

Sitomys keeni Rhoads, 1894:258.

Sitomys macrorhinus Rhoads, 1894:259.

Peromyscus keeni Bangs, 1897:75.

Peromyscus sitkensis Merriam, 1897:223.

Peromyscus oreas Bangs, 1898b:84.

Peromyscus prevostensis Osgood, 1901b:29.

Peromyscus hylaeus Osgood, 1908:141.

Peromyscus maniculatus oreas Osgood, 1909:51.

Peromyscus maniculatus hylaeus Osgood, 1909:53.

Peromyscus maniculatus keeni Osgood, 1909:55.

Peromyscus maniculatus algidus Osgood, 1909:56.

Peromyscus maniculatus macrorhinus Osgood, 1909:57.

Peromyscus sitkensis prevostensis Osgood, 1909:102.

Peromyscus maniculatus interdictus Anderson, 1932:110.

Peromyscus sitkensis oceanicus Cowan, 1935:432.

Peromyscus sitkensis isolatus Cowan, 1935:434.

Peromyscus maniculatus prevostensis McCabe and Cowan, 1945:187

Peromyscus maniculatus isolatus McCabe and Cowan, 1945:194.

Peromyscus maniculatus cancrivorus McCabe and Cowan, 1945:195.

Peromyscus maniculatus doylei McCabe and Cowan, 1945:196

Peromyscus maniculatus rubiventer McCabe and Cowan, 1945:196

Peromyscus maniculatus balaclavae McCabe and Cowan, 1945:197

Peromyscus maniculatus maritimus McCabe and Cowan, 1945:199

Peromyscus maniculatus pluvialis McCabe and Cowan, 1945:199

Peromyscus maniculatus triangularis Guiguet, 1955:B69.

Peromyscus maniculatus sartinensis Guiguet, 1955:B69.

Peromyscus maniculatus beresfordi Guiguet, 1955:B71.

Peromyscus maniculatus carli Guiguet, 1955:B72.

Holotype.—Academy of Natural Sciences, Philadelphia (catalog number 7,768); young adult, male, preserved as alcohol except skull. Original number 768 from the collection of S. N. Rhoads.

Type locality.—Canada: British Columbia; Masset, Graham Island, Queen Charlotte Islands; collected 1892 by J. H. Keen.

Subspecies.—Although we were not able to examine many of the subspecies that potentially are referable to *P. keeni*, based on the results of Hogan et al. (1993) and those presented herein, as well as distributional data presented in Hall (1981) we tentatively assign the following 22 subspecies recognized to *P. keeni*: *algides*, *angustus*, *balaclavae*, *beresfordi*, *cancrivorus*, *carli*, *doylei*, *georgiensis*, *hylaeus*, *interdictus*, *insolatus*, *keeni*, *macrorhinus*, *maritimus*, *oreas*, *oceanicus*, *pluvialis*, *prevostensis*, *rubiventer*, *sartinensis*, *sitkensis*, and *triangularis*.

Diagnosis.—Sides russet with darker brown on upperparts, underparts white. Skull heavy for the genus; nasal and rostrum short and thick; posterior nasal endings usually equaling premaxillae (Osgood 1909). Size is large for species group. Measurements obtained from Osgood (1909) and Allard and Greenbaum (1988), for several of the subspecies now assigned to *P. keeni*, indicate that the total length averaged 197.5 mm; (range 178–217 mm) and tail length averaged 103 mm (range 89–117 mm).

Examination of *Cyt*b sequences obtained in this study indicated that *P. keeni* differs from *P.* sp., *P. gambelii*, and *P. sejugis* (three closely related species to *P. keeni*) by 4.66%, 3.71%, and 3.97% respectively. Genetic differentiation (= 0.93%) based on DNA sequences obtained from 142 individuals of *P. keeni* indicated a low level of genetic divergence for members of the *P. maniculatus* species group. This species exhibited a similar level of genetic divergence as did *P. gambelii* and *P. labecula*, two species that occupy a similar-sized geographic area.

Distribution.—Occurs in the coastal regions (west of the Coastal and Cascade mountain ranges) in southern Alaska southward to central Washington (Hall 1981; Hogan et al. 1993; Gunn 1988; Gunn and Greenbaum 1986; Allard et al. 1987; Calhoun and Greenbaum 1991; Zheng et al. 2003; Lucid and Cook 2004). *P. keeni* also occurs on most of the islands in the Queen Charlotte Sound (coastal region of British Columbia) and the Alexander Archipelago (southwestern coast Alaska).

Comparison.—A member of the *P. maniculatus* species group. Morphological analyses (Gunn and Greenbaum 1986) indicate that samples of *P. oreas* (now referred to as *P. keeni*) were significantly larger than *P. m. austerus* (now referred to as *P. sonoriensis*), another species that occurs in the Pacific Northwest, in three external measurements including: total length, length of tail, and length of hindfoot (*P. keeni*; = 199.4 mm, 106.5 mm, and 22.5 mm and *P. sonoriensis*; = 175.7 mm, 85.4 mm, and 20.7 mm, respectively).

Similarly, Allard et al. (1987) indicated that 21 of 28 samples of *P. oreas* (now referred to as *P. keeni*) were significantly larger than those of *P. m. austerus* (now referred to as *P. sonoriensis*). In areas where *P. keeni* and *P. maniculatus* occur in sympatry, *P. keeni* are a habitat specialist (Songer et al. 1997) preferring a more old-growth forest habitat; whereas *P. maniculatus* prefer clear cut areas.

Remarks.—One hundred-eighty samples examined in this study were assigned to *P. keeni*. Of these samples, one from the southern portion of Prince of Wales Island, was approximately 100 km from the type locality on Queen Charlotte Island. Several studies (Robbins and Baker 1981; Rogers et al. 1984; Allard et al. 1987; Gunn and Greenbaum 1986; Calhoun and Greenbaum 1991; Hogan et al. 1993; Chirhart et al. 2001, 2005; Zheng et al. 2003), based on chromosomal, allozymic, morphologic, and sequence data, support a distinction between *P. keeni* (formerly recognized as *P. oreas* and *P. sitkensis*) and *P. sonoriensis* (formerly recognized as populations of *P. maniculatus*).

Gunn (1988), Gunn and Greenbaum (1986), and Hogan et al. (1993) reported two karyotypic groups of deermice from the Pacific northwest; a high FN 85–92 group that corresponded to *P. oreas* (now recognized as *P. keeni*) and a low FN group 74–78 that were assignable to *P. maniculatus*. No intermediate karyotypes were identified between these groups and individual mice with a high FN (85–92) typically possessed a large body size; whereas, mice with a low FN (74–78) typically possessed a smaller body size. As a result of these studies, populations formerly assigned to *P. oreas* and *P. sitkensis* were subsumed into *P. keeni* (Hogan et al. 1993).

Divergence estimates obtained herein suggested that *P. keeni* diverged, perhaps (weakly supported node), from the common ancestor of the unnamed species (*P.* sp. from the Yukon region) approximately 1.12 mya. Further it appears that the *P. keeni*/*P.* sp. lineage diverged from the other extreme western forms formerly assigned to *P. maniculatus* (*P. gambelii* and *P. sejugis* approximately 1.55 mya.

Peromyscus labecula (Elliot)

Peromyscus labecula Elliot, 1903:143.

Peromyscus sonoriensis blandus Osgood, 1904:56.

Peromyscus sonoriensis fulvus Osgood, 1904:57.

Peromyscus maniculatus fulvus Osgood, 1909:86.

Peromyscus maniculatus labecula Osgood, 1909:87.

Holotype.—Field Museum of Natural History (catalog number 8693), skin, skull, adult, sex unknown.

Type locality.—Ocotlán, Jalisco, Mexico; collected June 1901 by F. E. Lutz.

Subspecies.—Based on data obtained herein, we tentatively assign the following three subspecies recognized in Hall (1981) to *P. labecula*: *P. m. blandus*, *P. m. fulvus*, and *P. m. labecula*. It is possible that specimens from western Chihuahua, Mexico that were depicted by Hall (1981) as *P. m rufinus* (herein referred to *P. sonoriensis*) could be assigned to *P. labecula*. Samples from western Chihuahua, Mexico are needed to resolve this issue.

Diagnosis.—Upperparts pale (gray in winter), whitish, vinaceous buff and lined with dusky, occasionally russet; underparts white; ears dusky; tail sharply bicolored, brown above and white below (Osgood 1909). Size small to medium for species group; measurements obtained from Osgood (1909), for several of the subspecies now assigned to *P. labecula*, indicated a total length averaging 166 mm; (range 145–183 mm) and tail length averaging 70.5 mm (range 59–82 mm).

Genetically (mitochondrial DNA sequences; Dragoo et al. 2006; Kalkvik et al. 2012), *P. labecula* (specifically, samples referable to *P. l. blandus*) have been shown to differ from other populations formerly assigned to *P. maniculatus* from the southwestern United States (now referable to *P. sonoriensis*) as well as other regional members of the *P. maniculatus* species group now assigned to *P. melanotis* and *P. sejugis*. In this study, *Cyt*b sequences indicated that *P. labecula* differed from *P. gambelii*, *P. maniculatus* (*sensu stricto*), *P. melanotis*, *P. sejugis*, and *P. so-*

noriensis, by 3.80%, 3.79%, 5.90%, 4.22%, and 4.28%, respectively. Genetic differentiation (= 0.70%) based on DNA sequences obtained from 11 individuals of *P. labecula* was among the lowest intraspecific values obtained in this study; however, given the small sample size, the level of genetic divergence may have been under-estimated.

Distribution.—Lower Sonoran Zone of southern New Mexico and southwestern Texas, southward from east-central Chihuahua (perhaps western Chihuahua, see above) and western edge of Tamaulipas, and southward to Colima, Veracruz, and northern Oaxaca.

Comparisons.—A member of the *P. maniculatus* species group. Phenotypically resembles other species in terms of size, coloration, and bicolored tail. Averaging smaller than *P. sonoriensis* and tail shorter (< 75 mm); color more vinaceous. *P. labecula* can be distinguished from *P. melanotis*, with which it overlaps in distribution (the two species are separated by elevation), by larger body and lighter pelage (Osgood 1909).

Remarks.—Thirteen samples were examined in this study that are assignable to *P. labecula*. Of these samples, the closest examined herein was approximately 60 km northeast of the type locality in Ocotlán, Jalisco, Mexico.

Chromosomal variation reported for the three subspecies of *P. labecula* ranges from FN = 82–86 (Bowers et al. 1973; Peppers et al. 1997) with *P. l. fulvus* and *P. l. labecula* being reported as monomorphic (FN = 84; Bowers et al. 1973; Peppers et al. 1997) and *P. l. blandus* being polymorphic (FN = 82, 84, and 86; Bowers et al. 1973). The FNs reported for *P. labecula* fall within the upper ranges for reported for *P. gambelii*, *P. maniculatus*, and *P. sonoriensis* (see Table 2); but differed substantially from those observed for *P. melanotis* (FN = 62, Hsu and Arrighi 1968; Bowers et al. 1973), *P. polionotus* (FN = 69–71, Te and Dawson 1971), and *P. sejugis* (FN = 76, Smith et al. 2000).

Recognition of *P. labecula* as a species is supported by the analyses depicted in Dragoo et al. (2006), Gering et al. (2009), Kalkvik et al. (2012), Natarajan et al. (2015), and Kingsley et al. (2017) which showed a distinct lineage corresponding to samples residing in southern New Mexico, Texas, and Mexico. DNA sequence data (*Cytb*) and conformity to the Genetic Species Concept (see Bradley and Baker 2001; Baker and Bradley 2006) support elevation to species status. Although support for a *P. labecula*/*P. maniculatus* clade was weak, divergence time estimates indicated that *P. labecula* separated from *P. maniculatus* (*sensu stricto*) approximately 1.28 mya. The divergence of the *P. labecula*/*P. maniculatus* (*sensu stricto*) from a common ancestor that gave rise to *P. polionotus* and *P. sonoriensis* occurred approximately 1.56 mya, suggesting a rapid appearance of these four species with all four species appearing between 1.28 and 1.40 mya.

As discussed earlier, *P. labecula* appears to be sympatric with samples of *P. sonoriensis* in southcentral New Mexico (6.2 mi NW of Timberon). Additional data are need from these areas to determine if these genetic species (see Bradley and Baker 2001; Baker and Bradley 2006) are behaving as biological species (Mayr 1942) as well as genetic species.

Peromyscus maniculatus (Wagner)

Hesperomys maniculatus Wagner, 1845:148.

H[esperomys] gracilis Le Conte, 1855:442.

[*Hesperomys*] *arcticus* Coues, 1877:61,67.

Sitomys americanus canadensis Miller, 1893:55.

Peromyscus leucopus nubiterrae Rhoads, 1896:187.

Peromyscus canadensis abietorium Bangs, 1896:49.

Peromyscus canadensis umbrinus Miller, 1897:23.

Peromyscus maniculatus Bangs, 1898a:496.

Peromyscus canadensis argentatus Copeland and Church, 1906:122.

Peromyscus maniculatus gracilis Osgood, 1909:42.

Peromyscus maniculatus abietorium Osgood, 1909:45.

Peromyscus maniculatus argentatus Osgood, 1909:46.

Peromyscus maniculatus eremus Osgood, 1909:47.

Peromyscus maniculatus nubiterrae Osgood, 1909:47.

Peromyscus maniculatus anticostiensis Moulthrop, 1937:11.

Peromyscus maniculatus plumbeus C. F. Jackson, 1939:101.

Holotype.—Osgood (1909) reported that the type specimen resided in the Zoologischer Staatssammlung in Munich, although no catalog number or ancillary

data was provided. Specimens from the vicinity of Nain have been used for type location (Osgood 1909). Presumably collected by Wagner.

Type locality.—The exact type locality is not known; however, the Moravian settlements in Labrador, specimens from Nain have been used as the type location based on the interpretations of Osgood (1909).

Subspecies.—Although we were not able to examine all of the recognized subspecies that potentially are referable to *P. maniculatus*, we tentatively assign the following nine subspecies recognized in Hall (1981) to *P. maniculatus*: *abietorium*, *anticostiensis*, *argentatus*, *bairdi*, *eremus*, *gracilis*, *maniculatus*, *nubiterrae*, and *plumbeus*.

Diagnosis.—Size is large for species group; measurements obtained from Osgood (1909), for several of the subspecies now assigned to *P. maniculatus*, indicated a total length averaging 187 mm; (range 174–200 mm) and tail length averaging 91.5 mm (range 79–104 mm). Coloration is based on synopsis of Osgood's (1909) observations of several subspecies - back and sides are dark brown and tinged with fawn (varies among subspecies); venter is white; ears are dusky with pale edges; and tail is bicolored (brownish black above and white underneath).

Genetically (mitochondrial sequences; Dragoo et al. 2006; Kalkvik et al. 2012), *P. maniculatus* (specifically, samples referable to *P. m. abietorium*, *P. m. bairdi*, *P. m. gracilis*, *P. m. plumbeus*, *P. m. maniculatus*, and *P. m. nubiterrae*) have been shown to differ from other populations formerly assigned to *P. maniculatus* from the southwestern and central United States (*P. sonoriensis* – see above; and *P. polionotus*). In this study, *Cyt*b sequences indicated that *P. maniculatus* differed from *P. gambelii*, *P. melanotis*, *P. polionotus*, *P. sejugis*, and *P. sonoriensis*, by 4.90%, 6.65%, 5.12%, 5.40%, and 4.68%, respectively. Genetic differentiation (= 1.69%) based on DNA sequences obtained from 68 individuals of *P. maniculatus* was among the largest intraspecific values obtained in this study; however, *P. maniculatus* possesses one of the broadest geographic distributions of any taxon examined.

Distribution.—The distribution of *P. maniculatus* ranges from central Canada (Manitoba) eastward to Labrador then southward to Tennessee. It appears that populations of *P. maniculatus* are restricted to the eastern side of the Mississippi River. Samples from the western side of the Great Lakes area and boundaries of the provinces of Manitoba and Saskatchewan are needed to more accurately discern the boundaries of *P. maniculatus* and *P. sonoriensis* in this region.

Comparisons.—A member of the *P. maniculatus* species group. Phenotypically resembles other species in terms of size and coloration; although total and tail lengths are greater (typically 187 mm and 91.5 mm versus 151 mm and 65.5 mm, respectively) than in *P. sonoriensis* (populations west of the Mississippi River) and especially in comparison to *P. polionotus* (populations in the southeastern United States which average 130 mm and 47 mm, respectively).

Remarks.—One hundred-fourteen samples examined in this study were assigned to *P. maniculatus*. The type locality for *P. maniculatus* is unclear. Osgood (1909) interpreted the original type locality to be near the Moravian Settlements along the northeast coast of Labrador. In his revisionary work, Osgood (1909) included samples from Nain, Labrador as indicative of *P. maniculatus*. In this study, we also included two samples from Nain, Labrador; thereby following Osgood's lead for a consistent comparison of presumably the same taxon.

Chromosomal variation reported for two of the subspecies in *P. maniculatus* includes a broad range of FNs for *P. m. abietorum*, *P. m. anticostiensis*, *P. m. gracillis*, *P. m. maniculatus*, and *P. m plumbeus* (FN = 77, 82, 86–88; Singh and McMillian 1966; Myers Uncie et al. 1997). Clearly additional studies are needed to fill in the gaps for FNs that based on the current data, must range at least from 76 to 88. The FNs reported for *P. maniculatus* span the ranges for reported for *P. gambelii*, *P. labecula*, and *P. sonoriensis*; but differ substantially from those observed for *P. melanotis* (FN = 62, Hsu and Arrighi 1968; Bowers et al. 1973), *P. polionotus* (FN = 69–71, Te and Dawson 1971), and *P. sejugis* (FN = 76, Smith et al. 2000).

Recognition of *P. maniculatus* as a species, as outlined herein, is supported by the phylogenetic analyses of Dragoo et al. (2006) and Kalkvik et al. (2012) who suggested that a distinct lineage may occupy the

northeastern United States and eastern Canada. Additionally, Dragoo et al. (2006) reported that the greatest genetic divergence occurred between eastern clades and western clades. DNA sequence data (*Cyt*b) and conformity to the genetic species concept (see Bradley and Baker 2001; Baker and Bradley 2006) support elevation to species status. Divergence time estimates indicate that *P. maniculatus* (*sensu stricto*) diverged from *P. labecula* approximately 1.28 mya.

Peromyscus melanotis J. A. Allen and Chapman 1897

Peromyscus melanotis J. A. Allen and Chapman, 1897:203.

Holotype.—American Museum of Natural History (catalog number MO-10822); adult male; skin, skull, and skeleton. Original number 1,268 of Frank M. Chapman.

Type locality.—Mexico: Veracruz; Las Vigas; collected 23 April 1897.

Subspecies.—Recognized as a monotypic assemblage.

Diagnosis.—Size small for species group; measurements obtained from Osgood (1909) for several of the subspecies now assigned to *P. melanotis*, indicated a total length averaging 150 mm; (range 132–168 mm) and tail length averaging 62 mm (range 58–66 mm). Osgood (1909) further indicated that cranial measurements suggest a broad and more rounded braincase, auditory bulla is slightly smaller, and long rostrum. Pelage is very long, sides are a tawny ochraceous color.

Distribution.—Occurs in high elevation habitats in Chihuahua and southern Coahuila southward to Jalisco and central Veracruz (Hall 1981; Musser and Carleton 2005). Populations also occur in the upper montane regions in southern Arizona (Bowers et al. 1973).

Comparisons.—A species in the *P. maniculatus* species group. Morphologically similar to *P. labecula* (Osgood 1909), although smaller in overall length and tail length. Further, *Cyt*b sequences (this study) indicated that *P. melanotis* differs from *P. sonoriensis*, *P. gambelii*, *P. labecula*, and *P. sejugis* (four species in close geographic proximity to *P. melanotis*) by 6.02%, 5.31%, 5.90% and 4.80% respectively. Genetic differentiation (= 1.82%) based on DNA sequences obtained from five individuals of *P. melanotis* indicated one of the highest levels of genetic divergence for members of the *P. maniculatus* species group, despite the low sample size examined for this species.

Remarks.—Six samples were examined in this study that are assignable to *P. melanotis*. Of these samples, the closest examined herein was approximately 40 km (southwest of the type locality in Las Vigas, Veracruz.

Recognition of *P. melanotis* as a species, has been supported by phenotypic differences (Osgood 1909), ecology and elevation data (Álvarez-Castañeda 2005), unique chromosomal attributes (Bowers et al. 1973), allozyme data (Greenbaum et al. 1978; Avise et al. 1979; Rogers and Engstrom 1992), and molecular data (Hogan et al. 1997; this study). Blair (1950) suggested that *P. melanotis* is likely a peripheral isolate of *P. maniculatus* ancestral stock; a position that is supported by the unique and monomorphic karyotype (FN = 62, Bowers et al. 1973; Greenbaum et al. 1978).

Based on divergence time estimates and phylogenetic interpretations, it appears that *P. melanotis* is the most basal member of the *P. maniculatus* species group and diverged from all other members of the *P. maniculatus* species group approximately 1.98 mya. This date is the oldest date recovered for any member of the *P. maniculatus* species group.

Peromyscus polionotus (Wagner 1843)

Mus polionotus Wagner, 1843:52.

Hesperomys niveiventris (Chapman), 1889:18.

Sitomys niveiventris subgriseus Chapman, 1893:341.

Peromyscus phasma subgriseus Bangs, 1898c:199.

Peromyscus subgriseus subgriseus Bangs, 1898c:200.

Peromyscus subgriseus rhoadsi Bangs, 1898c:201.

Peromyscus subgriseus arenarus Bangs, 1898c:202-203.

Peromyscus subgriseus baliolus Bangs, 1898c:214-215.

Peromyscus polionotus Osgood, 1907:49.

Peromyscus polionotus niveiventris Osgood, 1909:105.
Peromyscus polionotus phasma Osgood, 1909:107.
Peromyscus polionotus rhoadsi Osgood, 1909:107.
Peromyscus polionotus albifrons Osgood, 1909:108.
Peromyscus polionotus leucophalus A. H. Howell, 1920:239.
Peromyscus polionotus decoloratus A. H. Howell, 1939:363.
Peromyscus polionotus peninsularis A. H. Howell, 1939:364.
P[eromyscus]. p[olionotus]. subgriseus Schwartz, 1954:562.
Peromyscus polionotus lucubrans Schwartz, 1954:564.
Peromyscus polionotus colemani Schwartz, 1954:566.
Peromyscus polionotus ammobates Bowen, 1968:16.
Peromyscus polionotus griseobaracatus Bowen, 1968:16.
Peromyscus polionotus trissyllepsis Bowen, 1968:17.
Peromyscus polionotus allophrys Bowen, 1968:18.
Peromyscus polionotus sumneri Bowen, 1968:20.

Holotype.—Osgood (1909) examined the type specimen (catalog number) on exhibit at the museum of the Polytechnic in Zurich. Skull and tail vertebrae were still in the specimen. The specimen initially was identified by Wagner (1843) as *Mus polionotus*, from somewhere in Georgia, United States. Osgood noted the identity of the specimen was most probably assignable to *P. p. subgriseus*.

Type locality.—Little information is available for determination of the type locality of *P. polionotus*. As researched and reviewed by Osgood (1909), it appears that Georgia, United States may be as precise a locality as is possible to determine.

Subspecies.—Hall (1981) recognized the following 16 subspecies: *P. p. albifrons*, *P. p. allophrys*, *P. p. ammobates*, *P. p. colemani*, *P. p. decoloratus*, *P. p. griseobaracatus*, *P. p. leucophalus*, *P. p. lucubrans*, *P. p. niveiventris*, *P. p. peninsularis*, *P. p. phasma*, *P. p. polionotus*, *P. p. rhoadsi*, *P. p. subgriseus*, *P. p. sumneri*, and *P. p. trissyllepsis*.

Diagnosis.—Size is very small for the species group (Osgood 1909). External measurements obtained from Osgood (1909), for several of the subspecies now assigned to *P. polionotus*, indicated a total length that ranged between 125–137 mm; (= 131 mm) and a tail length that ranged between 41–52 mm; (= 46.5 mm). Dorsal pelage is gray along back and shoulders with sides containing a mixture of gray and light cinnamon coloration. Tail is short and bicolored.

Distribution.—This species is restricted to the southeastern United States and ranges from northeastern Mississippi to western South Carolina, southward through Alabama and Georgia to central Florida (Osgood 1909).

Comparisons.—A member of the *P. maniculatus* species group. With the exception of slightly larger auditory bullae the skull is much smaller than other members of the genus and most closely resembles that of *P. maniculatus* (Osgood 1909; Hall 1981).

*Cyt*b sequences (this study) indicated that *P. polionotus* differs from *P. maniculatus* (*sensu stricto*) and *P. sonoriensis* by 5.12% and 4.71% respectively. Genetic differentiation (= 0.50%) based on DNA sequences obtained from 13 individuals of *P. polionotus* indicated the lowest level of genetic divergence for members of the *P. maniculatus* species group. The small geographic distribution of this species may explain this observation.

Remarks.—Thirteen samples were examined in this study that are assignable to *P. polionotus*. Of these samples, all were from Florida, given that the type locality is unknown we could not estimate the relative proximity; however, given that no other *P. maniculatus* species occurs in this area we assume these samples are good representatives of *P. polionotus*.

Although the karyotype of *P. polionotus* (FN = 69–71; Te and Dawson 1971) is unique relative to those of other species in the *P. maniculatus* group, several synapomorphies place it in this group (Robbins and Baker 1981; Stangl and Baker 1984). However, determining the phylogenetic association of *P. polionotus* to other members of the *P. maniculatus* species group has been problematic. Hooper (1968), and later Greenbaum et al. (1978), viewed *P. polionotus* to be an earlier peripheral isolate of grassland forms of *P. maniculatus* (*bairdi* and *pallescens*). Although allozyme and chromosome data (Greenbaum 1978; Avise et al. 1979; Robbins and Baker 1981; Stangl and Baker 1984) indicated that *P. polionotus* was sister to a clade containing taxa now

recognized as *P. sonoriensis* and *P. keeni*, Avise et al. (1983) suggested that *P. polionotus* was paraphyletic with *P. maniculatus* and that *P. polionotus* may represent a peripheral population of *P. maniculatus* that underwent speciation approximately 1.5 mya. Herein, this species is loosely allied (no nodal support) with clades I (*P. sonoriensis*), K (*P. maniculatus*), and L (*P. labecula*) but may have differentiated at a more recent date, approximately1.40 mya from the putative common ancestor with *P. sonoriensis* (Fig. 3).

Peromyscus sejugis Burt 1932

Peromyscus sejugis Burt, 1932:171.

Holotype.—California Institute of Technology (catalog number 50,632); adult male; skin and skull. Original number W. H. Burt 3,530.

Type locality.—Mexico: Baja California Sur; Santa Cruz Island, 25° 17'N, 110° 43'W; collected 23 January 1932.

Subspecies.—*P. sejugis* is monotypic.

Diagnosis.—Color of upperparts grayish with avellaneous and underparts white; tail bicolored with a narrow dorsal stripe. Skull arched antero-posteriorly; rostrum heavy; nasals broad, tapering posteriorly; relatively small auditory bullae (Burt 1932). Average measurements (Álvarez-Castañeda 2001): 160–197 mm; (= 184 mm) and a tail length that ranged between 65–94 mm; (= 85 mm). Larger in size than forms occurring on the mainland (specimens now assigned to *P. gambelii*), especially in total length (184 mm versus 164 mm) and tail length (85 mm versus 75 mm).

Distribution.—Known only from the Santa Cruz and San Diego Islands, Gulf of California, Mexico.

Comparisons.—A member of the *P. maniculatus* species group. Burt (1932) associated *P. sejugis* with *P. maniculatus* and noted that it was larger in size compared to *P. m. cooledgei* (now *P. gambelii*). The association with *P. gambelii* was confirmed based on phallic and allozyme data (Hooper and Musser 1964; Avise et al. 1979). Avise et al. (1979) implied that *P. sejugis* is as different from *P. maniculatus* (now *P. gambelii*) as it is from *P. melanotis* and *P. polionotus.* Hogan et al. (1997), Walker et al. (2006), and Greenbaum et al. (2017) reported low levels of mtDNA divergence between *P. sejugis* and *P. maniculatus* from Baja California but argued for retaining *P. sejugis* as a species based on unique morphometric and genetic characters (see *Remarks* below).

*Cyt*b sequences (this study) indicated that *P. sejugis* differs from *P. gambelii*, *P. keeni*, *P. labecula*, and *P. sonoriensis* by 2.05%, 3.97%, 4.42%, and 4.42%, respectively. Given the sample of one individual, within species genetic variation could not be determined.

Remarks.—A single sample was examined in this study that is assignable to *P. sejugis*. The specimen included herein was obtained from Mexico: Baja California Sur; Santa Cruz Island which is the type locality for *P. sejugis*.

Based on our examination of only a single individual, and the unclear phylogenetic results obtained herein due to the fact that our sample of *P. sejugis* was paraphyletic with samples representing *P. gambelii*, we defer to the findings and synopses offered in Walker et al. (2006) and Greenbaum et al. (2017) who opined that based on the available data, it was best to retain *P. sejugis* as a species. Specifically, they presented six reasons for continuing to recognize *P. sejugis* as a species separate from mainland forms of *P. maniculatus* (referred to *P. gambelii* by Greenbaum et al. 2017). First, morphological evidence presented by Burt (1932) and Álvarez-Castañeda (2001) depicted external and cranial differences between samples of *P. sejugis* and mainland forms. Second, Avise et al. (1974) reported allozymic differentiation between *P. sejugis* and mainland populations. Third, Smith et al. (2000), documented the appearance of a unique chromosomal inversion in *P. sejugis*. Fourth, Chirhart et al. (2005) reported a unique microsatellite allele in *P. sejugis*. Fifth, studies of mitochondrial DNA sequences (Hogan et al. 1997; Walker et al. 2006; Cornejo-Latorre et al. 2017; Greenbaum et al. 2017) depicted samples of *P. sejugis* and *P. maniculatus* to form monophyletic clades, respectively. Sixth, given previous lines of evidence and based upon the insular and restricted distribution of *P. sejugis*; as well as the surrounding conservation implications, demands careful treatment.

Our data indicate that *P. sejugis* is allied closely with *P. gambelii*, similar to results generated in Greenbaum et al. (2017). Genetic distance data generated herein suggest these populations diverged from *P. gambelii* found on Baja California Sur approximately between 0.44 and 0.67 mya (see Fig. 3).

Peromyscus sonoriensis (LeConte)

Hesp[*eromys*] *sonoriensis* Le Conte, 1853:413.

Hesperomys austerus Baird, 1855:336.

Mus bairdii Hoy and Kennicott, 1857:92.

Hesperomys sonoriensis var. *nebrascensis* Coues, 1877:79.

Hesperomys leucopus arcticus Mearns, 1890:285

Hesperomys leucopus nebrascensis Mearns, 1890:285.

Hesperomys leucopus deserticolus Mearns, 1890:287.

Hesperomys leucopus rufinus Merriam, 1890:65.

Peromyscus texanus nebrascensis J. A. Allen, 1896:251.

Sitomys americanus artemisiae Rhoads, 1894:260.

Sitomys insolatus Rhoads, 1894:256.

Peromyscus michiganensis pallescens J. A. Allen, 1896:238.

Peromyscus texanus saturatus Bangs, 1897:75.

Peromyscus texanus subarcticus J. A. Allen, 1899:15.

Peromyscus akeleyi Elliot, 1899:226.

Peromyscus maniculatus arcticus Osgood, 1900:33.

Peromyscus oreas rubidus Osgood, 1901a:193.

Peromyscus perimekurus Elliot, 1903:156.

Peromyscus oresterus Elliot, 1903:159.

Peromyscus luteus Osgood, 1905:77.

Peromyscus maniculatus artemisiae Osgood, 1909:58.

Peromyscus maniculatus saturatus Osgood, 1909:61.

Peromyscus maniculatus hollisteri Osgood, 1909:62.

Peromyscus maniculatus austerus Osgood, 1909:63.

Peromyscus maniculatus rubidus Osgood, 1909:65.

Peromyscus maniculatus rufinus Osgood, 1909:72.

Peromyscus maniculatus nebrascensis Osgood, 1909:75.

Peromyscus maniculatus luteus Osgood, 1909:77.

Peromyscus maniculatus bairdi Osgood, 1909:79.

Peromyscus maniculatus pallescens Osgood, 1909:83.

Peromyscus maniculatus sonoriensis Osgood, 1909:89.

Peromyscus maniculatus borealis Mearns, 1911:102.

Peromyscus maniculatus nebrascensis Mearns, 1911:102.

Peromyscus maniculatus osgoodi Mearns, 1911:102.

Peromyscus maniculatus angustus Hall, 1932:423.

Peromyscus maniculatus ozarkiarum Black, 1935:144.

Peromyscus maniculatus gunnisoni Goldman, 1937:224.

Peromyscus maniculatus alpinus Cowan, 1937:215.

Peromyscus maniculatus georgiensis Hall, 1938:455.

Peromyscus maniculatus serratus Davis, 1939:290.

Peromyscus maniculatus inclarus Goldman, 1939:355.

Peromyscus maniculatus bairdii McCabe and Cowan, 1945:197.

Peromyscus maniculatus saxamans McCabe and Cowan, 1945:198.

Holotype.—United States National Museum (catalog number 146); adult, sex unknown, skin and skull.

Type locality.—Mexico; Sonora; Santa Cruz; collected on 28 September 1851 by J. H. Clark.

Subspecies.—Although we were not able to examine all of the recognized subspecies that potentially are referable to *P. maniculatus*, we tentatively assign the following 15 subspecies recognized in Hall (1981) and Hogan et al. (1993) to *P. sonoriensis*: *alpinus*, *artemisiase*, *austerus*, *borealis*, *hollisteri*, *inclarus*, *luteus*, *nebrascensis*, *ozarkiarum*, *pallescens*, *rubidus*, *rufinus*, *saturatus*, *saxamans*, *serratus*, and *sonoriensis*.

Diagnosis.—Coloration varies greatly between subspecies (*austerus* darker in color whereas *pallescens* is much paler than other subspecies), however, most adults are ochraceous buff (Osgood 1909). Size small for species group, especially relative to length of the tail; measurements obtained from Osgood (1909) for several of the subspecies now assigned to *P. sonoroensis*, indicated a total length averaging 151 mm; (range 126–176 mm) and tail length averaging 65.5 mm (range 56–75 mm). Tail tends to be more thickly haired and more sharply bicolored (Osgood 1909) than other species in the group.

In this study, *Cyt*b sequences indicated that *P. sonoriensis* differed from *P. gambelii*, *P. melanotis*, *P. polionotus*, *P. sejugis*, and *P. maniculatus* (*sensu stricto*), by 4.55%, 6.02%, 4.71%, 4.42%, and 4.68%,

respectively. Genetic differentiation (= 1.27%) based on DNA sequences obtained from 186 individuals of *P. sonoriensis*. This species exhibited a moderate level of genetic divergence even though it possesses the broadest geographic distribution of the *P. maniculatus* species group.

Distribution.—Occurs primarily west of the Mississippi River from the Yukon and Northwest Territory southward to northern California and the United States/Mexico border (along Arizona and New Mexico) then eastward across northern Texas to Arkansas. The distribution of *P. sonoriensis* does not include: 1) the coastal islands and mainlands from Alaska southward to Oregon; in this area *P. keeni* may exclude *P. sonoriensis* or the two species may be sympatric; 2) southcentral California and Baja California and the southwest corner of Arizona where *P. gambelii* occurs; and 3) southern New Mexico, and southwestern of Texas where *P. labecula* occurs. Populations of mice that are assignable to *P. sonoriensis* appear to occur on Isle Royale, Michigan (Dragoo et al. 2006; this study) and in southern Michigan (Lansman et al. 1983); whereas samples from northcentral Michigan are assignable to *P. maniculatus* (Lansman et al. 1983). Additional samples are needed from much of the Great Lakes region to resolve this conundrum.

Comparisons.—A member of the *P. maniculatus* species group. Similar in coloration but smaller in size compared to other members of the *P. maniculatus* species group. Specimens from the Pacific Northwest are darker in pelage color (more similar to *P. keeni*) than those occurring in the central and eastern portions of the continent exhibit. Differs from *P. keeni* in external measurements such as tail length (averaging < 100 mm compared to an average length > 100 mm in *P. keeni*).

Remarks.—Two seventy-two samples examined were assigned to *P. sonoriensis*. Of these samples, the closest examined herein (Grant County, New Mexico) was approximately 200 km northeast of the type locality in Santa Cruz, Sonora.

Chromosomal data are highly variable for this group with a broad range of FNs (72–86) with some well-studied subspecies, such as *P. m. bardii*, reported as highly polymorphic (74–85). A trend in the data suggest that lower FNs (72–80) for this species occur in the Pacific Northwest, where populations exist in sympatry with *P. keeni* (Gunn and Greenbaum et al. 1986; Gunn 1988; Hogan et al. 1993). The FNs reported for *P. sonoriensis* span the ranges reported for *P. gambelii*, *P. labecula*, and *P. maniculatus*; but differ substantially from those observed for *P. melanotis* (FN = 62, Hsu and Arrighi 1968; Bowers et al. 1973), *P. polionotus* (FN = 69–71, Te and Dawson 1971), and *P. sejugis* (FN = 76, Smith et al. 2000).

Several previous studies (Dragoo et al. 2006, Gering et al. 2009, Kalkvik et al. 2012, Natarajan et al. 2015, Sawyer et al. 2017, and Greenbaum et al. 2017 indicated that populations of *P. maniculatus* in the eastern regions of the United States were genetically divergent from central and western populations. Similarly, DNA sequence data (*Cyt*b gene), presented herein, suggest elevation to species status that would include 17 currently recognized subspecies of *P. maniculatus*. This population encompasses the largest geographic area of any clade recovered in this study. Divergence dates suggest *P. sonoriensis* last shared a common ancestor with the lineage giving rise to *P. polionotus* approximately 1.40 mya.

As discussed earlier, *P. sonoriensis* appears to be sympatric with samples of *P. gambelii* in western Nevada (NAS Fallon Air Force Base) and at two separate localities in east-central California (one in Mono County and one in Tuolumne County). Further, *P. sonoriensis* appears to be sympatric with samples of *P. labecula* in southcentral New Mexico (6.2 mi NW of Timberon). Additional data are need from these areas to determine if these genetic species (see Bradley and Baker 2001; Baker and Bradley 2006) are behaving as biological species (Mayr 1942) as well as genetic species.

***Peromyscus* sp.**

Currently, there is not a definitive name available for populations from the southwestern Yukon region that were found to be distinct from other members of the *P. maniculatus* species group by Wike (1998), Lucid and Cook (2007), and this study. The Yukon specimens genetically are different from populations of *P. keeni* to the south and from populations of *P. maniculatus*-like

forms to the southwest and southeast that are now referable to *P. sonoriensis*. Wike (1998) eludes to the fact that the name *P. arcticus* might serve as a valid name for this distinct taxon. Although initially described as *Hesperomys leucopus arcticus* (Mearns 1890:285), this taxon later was treated as a subspecies, *Peromyscus maniculatus arcticus* (Osgood 1900:33). Later, Mearns (1911), based on "opinion 4" by the International Commission of Zoological Nomenclature (1910) realized that *P. m. arcticus* represented a preoccupied name that had been proposed by Coues (1877). Further, Mearns (1911) recognized that *P. m. arcticus* was problematic since the name referred to a specimen from Labrador (presumably assignable to a taxon from eastern Canada; most likely *P. m. maniculatus*); consequently, he described a new taxon (*P. m. borealis*) for the Yukon material and subsumed *P. m. arcticus* under this new subspecies and lists Fort Simpson, Yukon Territory, Canada as the type locality.

Based on the data presented by Wike (1998), Lucid and Cook (2007), and this study, the situation is further complicated by the fact that populations formerly referred to *P. m. borealis* are now assigned to *P. sonoriensis* (e.g. *P. s. borealis*). In fact, some of the samples, included herein (those assignable to *P. s. borealis*) are located only 235 km from the type locality of *P. s. borealis* at Ft Simpson, Yukon Territory; whereas the closest population of the seemingly new species (*P.* sp.; Lapie River; 8.5km West of Ross River) is located nearly 600 km to the west. However, it does not seem appropriate, at this time, to simply refer this new identified species to *P.* sp. until addition specimens in the vicinity of the type locality of *P. s. borealis* can be examined. Therefore, we have not provided a formal description for the putative new species; instead we off a brief discussion of how it differs, genetically, from the two species (*P. sonoriensis* and *P. keeni*) that geographically are in close proximity to *P.* sp.

Justification for a new taxon.—Examination of *Cyt*b sequences obtained in this study indicated that *P.* sp. differs from *P. sonoriensis* and *P. keeni* (two species geographically located to *P.* sp.) by 4.80% and 4.66% respectively. Genetic differentiation (= 0.92%) based on DNA sequences obtained from 28 individuals of *P.* sp. indicated a low level of genetic divergence for members of the *P. maniculatus* species group. This species exhibited a similar level of genetic divergence as did *P. gambelii* and *P. labecula*; two species that also occupy a fairly restricted geographic area.

Distribution of P. *sp.*—Occurs in the southwestern portion of the Yukon province (Wike 1998; Lucid and Cook 2004; Sawyer et al. 2017; this study). Specifically, it appears that *P.* sp. is distributed along the lower elevations associated with the western portion of the Klondike and Yukon Plateaus, bounded by the Ogilvie Mountains in the north, the Saint Elias Mountains to the south, and Pelly Mountains to the east. Further it appears that *P. sonoriensis* occupies the regions to the northeast and southwest of Haines Junction; whereas *P. keeni* is distributed further to the east and south. Further collecting in the southern Yukon is necessary to determine the distributions of the three species (*P. keeni*, *P. sonoriensis* and *P.* sp.) occupying this area.

Remarks.—Thirty-eight samples examined in this study were assigned to *P.* sp. Genetic divergences detected among the three species (*P. keeni*, *P. sonoriensis*, and *P.* sp.) occupying the Yukon and surrounding areas are similar to those detected among other recognized species in the *P. maniculatus* (Hogan et al. 1997; Greenbaum et al. 2017; this study), *P. boylii* (Bradley et al. 2014, 2017), and *P. mexicanus* (Bradley et al. 2015) species groups; and considerably less than reported for the *P. truei* (Durish et al. 2004) species group. Further these results are in agreement with characteristics of genetic species as presented in Bradley and Baker (2001) and Baker and Bradley (2006). Divergence estimates obtained herein suggested that *P.* sp. diverged from a common ancestor of the *P. keeni* clade approximately 1.12 mya.

Evolutionary History, Divergence, and Distribution of Phylogroups

Patterns of evolutionary history, divergence, and distribution of phylogroups were inferred from the results of a molecular dating analyses (BEAST; Bouckaert et al. 2014) using DNA sequence data generated herein and from GenBank. Given that some clades can be collapsed due to lack of support, divergence values estimated in this section should be interpreted as minimal ages for each nodes C, G, and H. Data indicated that the ancestor to the *P. maniculatus*

species group diverged from the *P. leucopus* species group approximately 2.49 mya (Fig. 3) and in essence became the *P. maniculatus* species group approximately 1.98 mya (Fig. 4A). Cladogenesis within the *P. maniculatus* species group resulted from a series of events (between 0.44-0.96 mya) that gave rise to the nine species discussed herein (Figs. 3 and 4). These results are in agreement with other studies (Zheng et al. 2003; Dragoo et al. 2006; Van Zant and Wooten 2007; Platt et al. 2015a; Sawyer et al. 2017) that suggested the majority of diversification events within the *P. maniculatus* species group occurred during the Pleistocene.

Dragoo et al. (2006) reported that patterns of phylogeographical structure in *P. maniculatus* correspond to hypothesized Pleistocene expansion for other mammalian taxa (Hayes and Harrison 1992; Byun et al. 1997; Brant and Ortí 2003; Lessa et al. 2003; Runck and Cook 2005). Those studies examined variation in mtDNA sequences and uncovered genetic signals of postglacial colonization among members of distinct clades found in eastern and western regions of the continent (east and west of the Mississippi River). Data from those phylogeographic studies, coupled with data from geological literature (Dyke and Prest 1987; Tushingham and Peltier 1991; Dyke 2004) suggested that mammalian populations were isolated in refugia during the Pleistocene glacial periods and later expanded to their current distribution. Below, we briefly discuss the evolutionary history of the *P. maniculatus* species group and provide inferences relative to current distribution patterns. Based on the data presented herein, it is hypothesized that the ancestral form of *P. maniculatus* occupied a central portion of North America and that cladogensis, resulting either from vicariant events or adaptive radiations and subsequent dispersal, were responsible for modern day distributions (Fig. 4A–H).

P. melanotis.—The common ancestor to a *P. melanotis*-like ancestor diverged from the remained of the *P. maniculatus* species group 1.98 mya (Fig. 4B). This is in agreement with results obtained from studies of chromosomal evolution (Greenbaum et al. 1978; Robbins and Baker 1981) and phylogenetic analyses of DNA sequence data (Platt et al. 2015a). Currently, *P. melanotis* is distributed at high elevations (> 2,900 m) in the intermixed pine-fir and grassland habitats of the Sierra Madre Orientals, Sierra Madre Occidentals, Trans-Mexican Volcanic Belt, and the Chiricahua Mountains of southern Arizona (Carleton 1989; Álvarez-Castañeda 2005; Bowers et al. 1973). Although populations of *P. melanotis* in eastern, western, and southern Mexico are separated by the Central Mexican Plateau, genetic variation within the species (2.18%) indicated a level of connectivity among populations in the three montane regions, presumably as a result of geneflow across the southern portion of their distribution. Glaciation events associated with the Last Glacial Maximum of the Pleistocene (< 2 mya; Fa and Morales 1993; Marshall and Liebherr 2000) may have contributed to the current distributional pattern. In addition, Bowers et al. (1973) noted that similarities in habitat, karyotype, electrophoretic mobility patterns, and breeding data reflected genetic relationships between populations of *P. melanotis* in Arizona and Mexico, thereby suggesting that Arizona populations might represent a northern extension of Mexican populations.

*P. gambelii/sejugis/keeni/*sp.—The common ancestor to the lineage giving rise to *P. gambelii*, *P. sejugis*, *P.* sp. and *P. keeni* diverged approximately 1.55 mya, perhaps as a peripheral isolate, from a *P. maniculatus*-like ancestor now recognized as *P. sonoriensis* (Fig. 4C). The four present-day taxa subsequently arose 0.44–0.84 mya. This lineage occupied the coastal mountain ranges of western North America, including the area from present-day Alaska and the Yukon southward to Baja California Sur. The biogeography of this region is complicated by the potential influences of the many islands, rivers, and mountains and a thorough treatment is well beyond the scope of this study; however, Sawyer et al. (2017) provided a detailed synopsis of divergence times, ecological niche differentiation, and possible migration pathways for these four species.

P. polionotus.—The common ancestor to the species now recognized as *P. polionotus* appears to have diverged approximately 1.40 mya, perhaps as a peripheral isolate, from a *P. maniculatus*-like ancestor (Fig. 4D). Our summation is in agreement with the findings of Van Zant and Wooten (2007) who suggested that *P. polionotus* became isolated from its *P. maniculatus*-like ancestor >1 mya of as a result of temperature changes shifting vegetation zones in the Pleistocene. Currently,

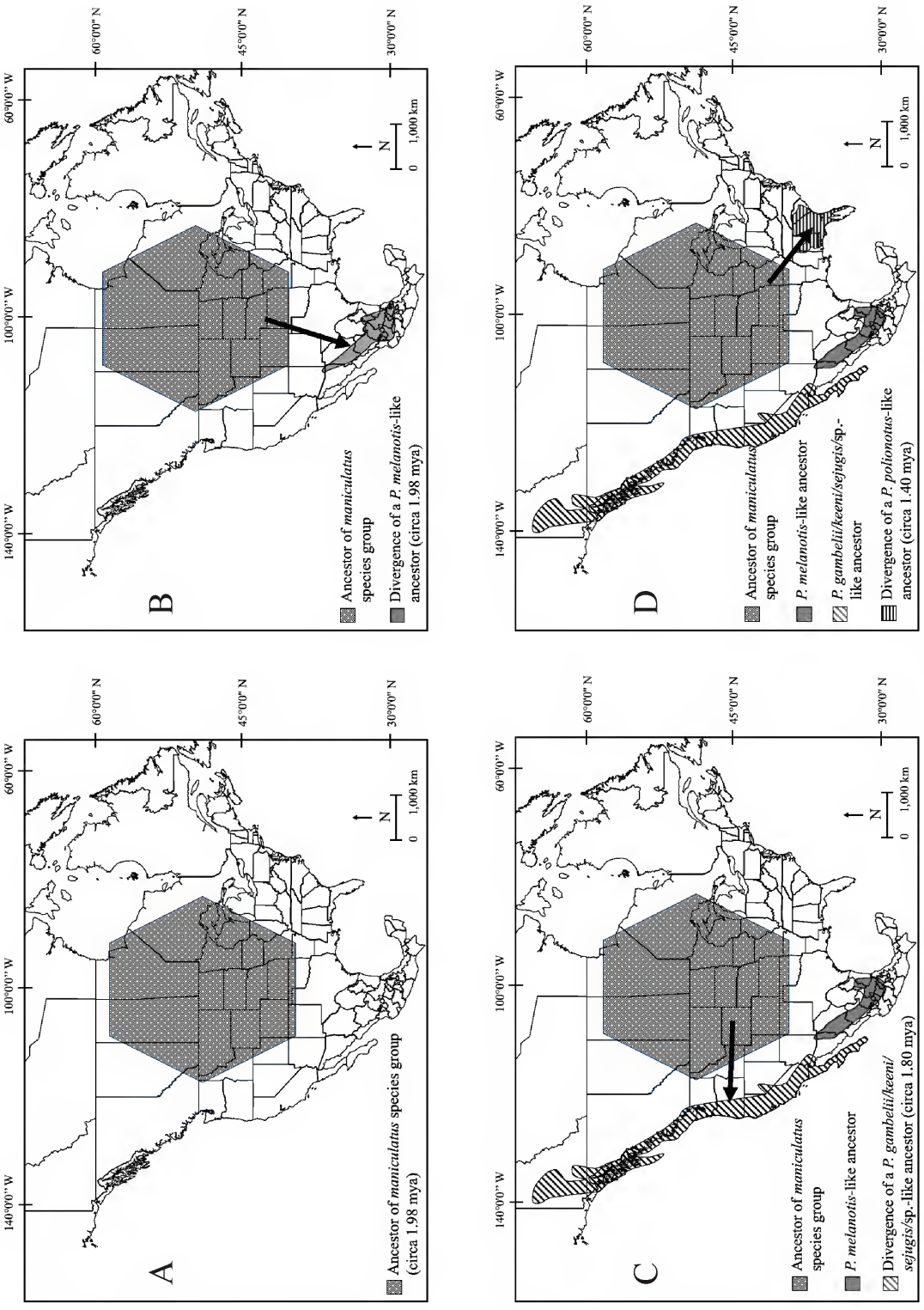

Figure 4. Approximate distributions and associated divergence times for A) *Peromyscus maniculatus*-like ancestor; B) *P. melanotis*-like ancestor; C) *P. gambelii/keeni/sejugis*/sp.-like ancestor; D) *P. polionotus*-like ancestor; E) *P. sonoriensis*-like ancestor; F) *P. labecula* and *P. maniculatus*-like ancestor; G) *P. keeni*/sp.-like ancestor; and H) P. *keeni*-like, *P. gambelii*-like, *P. sejugis*-like, and *P*. sp.-like ancestors. Divergence times were estimated from the BEAST analysis (Version 2.4, Bouckaert et al. 2014) of the mitochondrial cytochrome-*b* gene dataset (see Fig. 3). Shading schemes that correspond to species distributions are shown in the inset.

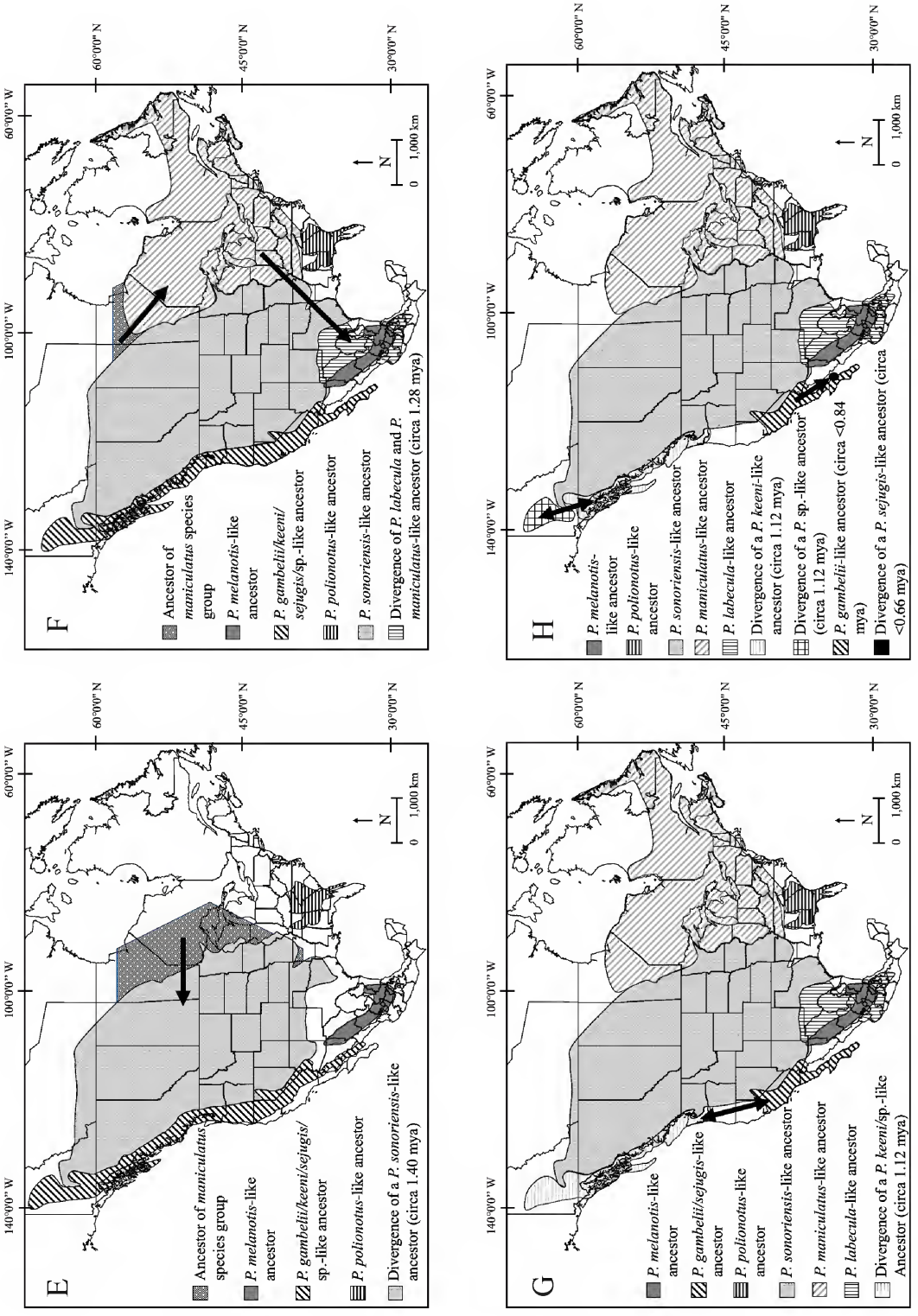

Figure 4. (cont.)

P. polionotus occupies the extreme southeastern portion of the United States (eastern edge of Mississippi through South Carolina and Florida). This region is well known as having served as a refugia, for many vertebrate species, as a result of the Laurentide ice sheet (Hewitt 2004).

P. sonoriensis.—The common ancestor to the lineage recognized as *P. sonoriensis* diverged from the common ancestor of a *P. polionotus*-like ancestor approximately 1.40 mya (Fig. 4E). Given the distribution of haplotypes recovered herein, it appears the Mississippi River may have played a vicariant role in isolating *P. sonoriensis*, to the west, from populations of the *P. maniculatus*-like ancestor to the east. Given the ebb and flow of ice sheets in North America, during the last one million years, it is likely that the Mississippi River was formidable barrier during warmer periods. One exception appears that involves samples from Isle Royale, Michigan. These samples from a region east of the Mississippi River grouped with *P. sonoriensis*, whereas samples from the closest geographic locations to Isle Royale (the upper peninsula of Michigan, northern Minnesota, and southern Ontario) cluster with *P. maniculatus* (*sensu stricto*). Our results are similar to that reported in Dragoo et al. (2006) and may indicate a more complex biogeographic history in the Great Lakes region. The southern distribution of *P. sonoriensis* occurs along the boundary of the Chihuahuan Desert and Rio Grande drainage with populations assignable to *P. sonoriensis* occurring north of that region, whereas populations assignable to *P. labecula* occur to the south. To the west, *P. sonoriensis* abuts the distributions of *P. keeni* (in the northwestern) and *P. gambelii* (in the southwest); presumably occupying the habitats east of the coastal mountain ranges; whereas, *P. keeni* and *P. gambelii* occur to the northwest and to the southwest, respectively. At this time, it is unclear how the distributions of *P. sonoriensis* and *P.* sp. are delimited in the Yukon region. It is likely that *P. sonoriensis* expanded into the low elevation regions of the northern Mojave and Great Basin deserts and surrounding areas after the last glacial maximum, similar to data generated in studies of other vertebrates (Mulcahy 2008; Jezkova et al. 2015).

P. labecula.—Based on divergence times estimated herein, it appears that *P. labecula* diverged from a shared common ancestor with *P. maniculatus* approximately 1.28 mya (Fig. 4F). Although analyses (Figs. 2 and 3) depict *P. labecula* as sharing a common ancestor with *P. maniculatus* it should be noted that nodal support for that arrangement was not recovered in any of the analyses. Therefore, *P. labecula*, *P. maniculatus*, *P. sonoriensis*, and *P. polionotus* should be viewed as an unresolved polytomy. The proposed divergence times for these four taxa (0.52 and 0.96 mya, Fig 3) suggest a rapid divergence and support the premise that is difficult to reconstruct the phylogenetic relationships among these four taxa. The distribution of *P. labecula*, which includes the Lower Sonoran Zone of southern New Mexico and southwestern Texas southward into the Mexican states of Chihuahua, Durango and western edge of Tamaulipas and southward to Colima, Veracruz, and northern Oaxaca, would suggest a possible shared ancestry with *P. sonoriensis* distributed to the immediate north.

P. keeni.—It appears that *P. keeni* split from a *P.* sp.-like ancestor approximately 1.12 mya (Fig. 4F); with *P. keeni* and *P.* sp. occupying the northern coastal and Yukon regions (Alaska southward to the San Francisco Bay region) and the *P. gambelii/sejugis*-like ancestor occupying the southern coastal areas (San Francisco Bay region southward to Baja California del Sur). These four species form a monophyletic group in other phylogenetic studies (Hogan et al. 1997; Lucid and Cook 2004; Chirhart et al. 2005; Dragoo et al. 2006; Gering et al. 2009; Kalkvik et al. 2012; Sawyer et al. 2017) confirming a shared evolutionary history. Lucid and Cook (2004) and Zheng et al. (2003) suggested that these genetic and phylogeographic relationships are a product of glacial refugia, with *P. keeni* surviving in an ice-free coastal refugia (see Hamilton 1994) in southeastern Alaska and British Columbia during the Late Pleistocene and expanding its range into the Pacific Northwest prior to the arrival of *P. maniculatus* (now recognized as *P. sonoriensis*). It appears that the distributions of *P. keeni* and the *P. gambelii/sejugis*-like ancestor were separated by ice sheets and pluvial lakes during the late Pleistocene (Grayson 1993; Reheis 1999; Hewitt 2004).

P. sejugis.—Divergence times estimated herein, indicate that *P. sejugis* diverged from *P. gambelii* approximately 0.44 to 0.67 mya (Fig. 4H). This finding,

based on a single DNA sequence, suggests a very recent evolutionary history for these two taxa. It appears that *P. sejugis* which occurs only on the Santa Cruz and San Diego Islands off the east coast of Baja California del Sur was isolated from mainland populations of *P. gambelii*. Fluctuations in sea levels during this time span resulted in the emergence and disappearance of land bridges that connected current islands to the mainland and potentially influencing the genetic structure of the biota inhabiting the Baja California Peninsula and surrounding islands (Álvarez-Castañeda and Murphy 2014; Dolby et al. 2015).

In conclusion, this study is intended to serve as a starting place and initial hypothesis for further testing species boundaries and distributional limits of taxa assigned to the *P. maniculatus* species group. Osgood (1909) and others (Hooper 1968; Carleton 1989) have outlined the complexities surrounding this group of deermice. Herein, DNA sequence data have been used in attempt to begin working toward a taxonomic resolution. It is clear that additional data are required to better test the phylogenetic interpretations and hypotheses presented in this study. First, although we examined as many samples and taxonomic groups (primarily subspecies) as were available in major systematic collections in the United States, many geographic regions and subspecies were not sampled. In particular, many of the insular forms along California and Baja California were not included. Probably hundreds of additional and critically located samples are needed to thoroughly test all phylogenetic hypotheses and potential distributional boundaries.

Second, we recognize that data from nuclear genes are necessary to substantiate the findings based on mtDNA sequences. Presumably, next generation methods such as targeted sequencing (ddRADseq - Gilman and Tank 2018; UCEs - Faircloth et al. 2013), genotyping rare genetic events (Platt et al. 2015b) mitochondrial (Sullivan et al. 2017) and eventually whole genome phylogenetics could be used in conjunction with a carefully planned sampling scheme to test the appropriateness of the proposed phylogroups and taxonomic distributions.

Third, several macro-evolutionary and biogeographic hypotheses are available for examination. For example, Greenbaum et al. (1978) posited that *P. maniculatus* represented an example of centrifugal speciation as described by Brown (1957). Under that scenario, *P. maniculatus* represented the central species, whereas *P. polionotus* and *P. melanotis* were peripheral isolates; *P. maniculatus* was therefore more likely to have greater variation than the peripheral species (Greenbaum et al. 1978). In contrast, Blair (1950) suggested that *P. maniculatus* represented the evolutionary stock that gave rise to other members of the *P. maniculatus* species group. Based on data generated herein, it may be that both positions are correct as a *P. maniculatus*-like ancestor appears to have given rise directly to five evolutionary lineages (*melanotis*, *keeni*/sp./*gambelii*/*sejugis*, *polionotus*, *sonoriensis*/sp., and *maniculatus*/*labecula*; see Fig 4) with only two lineages (*gambelii* and *sejugis*) diverging from a non-*P. maniculatus*-like ancestor. Although these events may have appeared as a result of peripheral isolation, addition data are needed to evaluate this hypothesis.

Fourth, and finally, *P. maniculatus* and its allies form one of the cornerstone taxonomic groups for numerous biological studies. If multiple, cryptic species exist within this wide-ranging taxon, then a refined taxonomic assessment could have a major impact across many biological disciplines.

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APPENDIX

Specimens examined in the DNA sequencing portion of this study are listed below by taxon. For each specimen, the abbreviated collecting locality (contact the respective natural history museum for a more complete listing of locality), GenBank accession number, museum catalog number (abbreviations for museum acronyms follow Dunnum et al. 2018) are provided. Abbreviations are as follows: Carnegie Museum of Natural History (CM and SP); Centro de Investigaciones Biológicas del Noroeste (CIB); Christopher L. Parkinson personal collecting number – no museum catalog number available (CLP); Instituto Politécnico Nacional, Colección Regional Durango (CRD); Jay F. Storz personal collecting number – no museum catalog number available (JFS); Monte L. Bean Life Science Museum (BYU); Museum of Southwestern Biology (MSB and NK); Museum of Texas Tech University (TTU and TK); Museum of Vertebrate Zoology, (MVZ), Oswego State University (OSM); University of Alaska Museum (UAM); University of Washington Burke Museum (UWBM); and no museum catalog number available (EAR, HGPeke, and WM).

Country	State/Province	Locality	GenBank	Museum
		Peromyscus gambelii		
Mexico	Baja California Sur	Santa Margarita Island, Naval Base	DQ385707	MSB 58325
Mexico	Baja California Sur	Santa Margarita Island, Naval Base	DQ385709	MSB 58326
Mexico	Baja California Sur	Santa Margarita Island, Naval Base	DQ385706	MSB 58328
Mexico	Baja California Sur	Santa Margarita Island, Naval Base	DQ385708	MSB 58330
USA	Arizona	1.3 mi S, 3.5 mi W Somerton	MH299891	TTU 81287
USA	California	Vandenberg Air Force Base	DQ385710	MSB 87462
USA	California	Vandenberg Air Force Base	DQ385711	MSB 87484
USA	California	Vandenberg Air Force Base	DQ385712	MSB 87485
USA	California	Vandenberg Air Force Base	DQ385713	MSB 87486
USA	California	Vandenberg Air Force Base	DQ385714	MSB 87492
USA	California	Arroyo Seco	EF666142	MVZ 186299
USA	California	Bear Ranch, Coyote Reservoir	EF666143	MVZ 200988
USA	California	La Grange	EF666144	MVZ 207832
USA	California	La Grange	EF666145	MVZ 207835
USA	California	Peaslee Creek	EF666147	MVZ 207843
USA	California	Merced River Ranch, Snelling	EF666148	MVZ 207844
USA	California	Merced River Ranch, Snelling	EF666149	MVZ 207845
USA	California	Merced River Ranch, Snelling	EF666150	MVZ 207846
USA	California	Kelsey Ranch, 5.2 mi E Snelling	EF666151	MVZ 207857
USA	California	Kelsey Ranch, 5.2 mi E Snelling	EF666152	MVZ 207859
USA	California	Kelsey Ranch, 1 km S Kelsey Res.	EF666153	MVZ 207863
USA	California	Upper Lyell Canyon, Yosemite NP	EF666154	MVZ 202229
USA	California	Upper Lyell Canyon, Yosemite NP	EF666156	MVZ 202235
USA	California	Upper Lyell Canyon, Yosemite NP	EF666157	MVZ 202236
USA	California	Upper Lyell Canyon, Yosemite NP	EF666158	MVZ 202243
USA	California	Upper Lyell Canyon, Yosemite NP	EF666159	MVZ 202246
USA	California	Upper Lyell Canyon, Yosemite NP	EF666160	MVZ 202249
USA	California	Upper Lyell Canyon, Yosemite NP	EF666164	MVZ 202264

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	California	Upper Lyell Canyon, Yosemite NP	EF666165	MVZ 202217
USA	California	E end Fletcher Lake, Yosemite NP	EF666166	MVZ 208025
USA	California	E end Fletcher Lake, Yosemite NP	EF666168	MVZ 208027
USA	California	E end Fletcher Lake, Yosemite NP	EF666169	MVZ 208028
USA	California	E end Fletcher Lake, Yosemite NP	EF666170	MVZ 208029
USA	California	E end Fletcher Lake, Yosemite NP	EF666171	MVZ 208032
USA	California	E end Fletcher Lake, Yosemite NP	EF666172	MVZ 208036
USA	California	Vogelsang Lake, Yosemite NP	EF666173	MVZ 208081
USA	California	Vogelsang Lake, Yosemite NP	EF666174	MVZ 208084
USA	California	Vogelsang Lake, Yosemite NP	EF666175	MVZ 208085
USA	California	Vogelsang Lake, Yosemite NP	EF666176	MVZ 208100
USA	California	Vogelsang Lake, Yosemite NP	EF666177	MVZ 208097
USA	California	Barcroft Research Station	EF666180	WM 3
USA	California	Barcroft Research Station	EF666181	WM 6
USA	California	Barcroft Research Station	EF666183	WM 8
USA	California	Barcroft Research Station	EF666184	WM 10
USA	Nevada	Naval Air Station Fallon, 1,300 m	DQ385715	MSB 74965
		Peromyscus keeni		
Canada	British Columbia	Hotsprings Island (HTS)	KF949153	HGPeke 9701
Canada	British Columbia	Hotsprings Island (HTS)	KF949154	HGPeke 9702
Canada	British Columbia	Hotsprings Island (HTS)	KF949155	HGPeke 9703
Canada	British Columbia	Cassiar Hwy (Hwy 37), Slate Creek	KF949157	MSB 147720
Canada	British Columbia	Cassiar Hwy (Hwy 37), Slate Creek	KF949160	MSB 147719
Canada	British Columbia	Stikine River	KF949264	UAM 52680
Canada	British Columbia	Iskut River Valley	KF949291	UAM 52511
Canada	British Columbia	Iskut River Valley	KF949292	UAM 52518
Canada	British Columbia	Cassiar Hwy (Hwy 37), Slate Creek	KF949301	MSB 156119
Canada	British Columbia	Ramsay Island (RMS)	KF949302	HGPeke 306
Canada	British Columbia	Ramsay Island (RMS)	KF949303	HGPeke 307
Canada	British Columbia	Ramsay Island (RMS)	KF949304	HGPeke 308
Canada	British Columbia	Ramsay Island (RMS)	KF949305	HGPeke 309
Canada	British Columbia	Stikine River, Dodjatin Creek	KF949327	UAM 51070
Canada	British Columbia	Keogh Main Rd, 4.5 mi W Hwy 19	KF949332	UWBM 75393
Canada	British Columbia	Log Creek vicinity; N of Nahatlatch	KF949333	UWBM 75449
Canada	British Columbia	Log Creek vicinity; N of Nahatlatch	KF949334	UWBM 75450
Canada	British Columbia	Cassiar Hwy (Hwy 37), 1 km W Willow	KF949335	MSB 147174
Canada	British Columbia	Cassiar Highway (Hwy 37), Burrage Riv.	KF949336	MSB 155704
Canada	British Columbia	Cassiar Highway (Hwy 37), Rescue Riv.	KF949337	MSB 155836
Canada	British Columbia	Cassiar Highway (Hwy 37), Rescue Riv.	KF949338	MSB 155873
Canada	British Columbia	Cassiar Hwy (Hwy 37), Slate Creek	KF949339	MSB 156117

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
Canada	British Columbia	Tatshenshini River 114P, Chilkat Pass	KF949340	UAM 50570
Canada	British Columbia	Stikine River, mouth of Dodjatin Creek	KF949341	UAM 52661
Canada	British Columbia	Stikine River	KF949342	UAM 52664
Canada	British Columbia	Stikine River	KF949343	UAM 52665
Canada	British Columbia	Stikine River	KF949344	UAM 52666
Canada	British Columbia	Iskut River Valley	KF949346	UAM 52512
Canada	British Columbia	Iskut River Valley	KF949347	UAM 52516
Canada	British Columbia	Madeley Lake [Creek]; NW of Whistler	KF949353	UWBM 75463
Canada	British Columbia	Mamquam River; E of Squamish	KF949354	UWBM 75480
Canada	Yukon	4 Mile Fish Lake Rd, Whitehorse	KF949297	UAM 71620
Canada	Yukon	No specific locality recorded	KF949348	UAM 71580
Canada	Yukon	No specific locality recorded	KF949349	UAM 71581
Canada	Yukon	4 Mile Fish Lake Rd, Whitehorse	KF949350	UAM 71622
Canada	Yukon	No specific locality recorded	KF949351	UAM 71660
Canada	Yukon	Whitehorse	AY529417	UAM 71659
USA	Alaska	Bushy Island	AF119261	UAM 50770
USA	Alaska	Craig Quad, Alexander Archipelago, Dall	AY529316	UAM 73710
USA	Alaska	Prince of Wales Island, Nichols Lake	KF949158	UAM 23717
USA	Alaska	No specific locality recorded	KF949159	UAM 31102
USA	Alaska	Juneau; Smugglers cove	KF949256	MSB 157000
USA	Alaska	Coronation Island, Egg Harbor	KF949257	MSB 198221
USA	Alaska	Prince of Wales Island, Turn Creek, El	KF949258	UAM 74969
USA	Alaska	Revillagigedo Island, Ella Bay	KF949259	UAM 23443
USA	Alaska	Zarembo Island	KF949260	UAM 43440
USA	Alaska	Foggy Bay, Kirk Point	KF949263	UAM 23421
USA	Alaska	Mitkof Island, 0.75 mi S Blind Slough	KF949265	UAM 23104
USA	Alaska	Stikine River, Figure Eight Lake	KF949269	UAM 20698
USA	Alaska	Stikine River, Figure Eight Lake	KF949270	UAM 20949
USA	Alaska	Mitkof Island, 0.75 mi S Blind Slough	KF949271	UAM 23108
USA	Alaska	mouth of Unuk River	KF949272	UAM 23491
USA	Alaska	mouth of Unuk River	KF949273	UAM 23492
USA	Alaska	Heceta Island, Port Alice, Mint Lake	KF949274	UAM 23828
USA	Alaska	Heceta Island, Port Alice, Mint Lake	KF949275	UAM 23831
USA	Alaska	Baranof Island, Plotnikof Lake	KF949276	UAM 30818
USA	Alaska	Baranof Island, Plotnikof Lake	KF949277	UAM 30820
USA	Alaska	Warren Island, Warren cove	KF949278	UAM 31727
USA	Alaska	Warren Island, Warren cove	KF949279	UAM 31729
USA	Alaska	Etolin Island, Anita Bay	KF949280	UAM 34616
USA	Alaska	Forrester Island, Eagle Harbor	KF949281	UAM 42792
USA	Alaska	Forrester Island, Eagle Harbor	KF949282	UAM 42794

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Alaska	San Fernando Island	KF949283	UAM 42801
USA	Alaska	San Fernando Island, SE, near Ridge Isl.	KF949284	UAM 42831
USA	Alaska	Kosciusko Island, Charley Creek, Edna	KF949285	UAM 49629
USA	Alaska	Turner Lake	KF949286	UAM 50751
USA	Alaska	White Pass	KF949287	UAM 50800
USA	Alaska	Taiya River, mouth of W Branch	KF949288	UAM 50802
USA	Alaska	Chichagof Island, Salt Lake Bay	KF949289	UAM 50930
USA	Alaska	Chichagof Island, Salt Lake Bay	KF949290	UAM 50936
USA	Alaska	Haines Hwy: 3.9 mi WNW Haines	KF949293	UAM 52642
USA	Alaska	Gravina Island, Phocena Bay	KF949294	UAM 70143
USA	Alaska	Kosciusko Island, Charley Creek, Edna	KF949296	UAM 70204
USA	Alaska	Tlevak Narrows	KF949298	UAM 73830
USA	Alaska	Prince of Wales Island, Turn Creek, El	KF949299	UAM 74968
USA	Alaska	Kuiu Island, Rocky Pass, 1.5 km S.	KF949300	MSB 148974
USA	Alaska	Coronation Island, Egg Harbor	KF949306	MSB 198194
USA	Alaska	Noyes Island, E side	KF949307	MSB 221318
USA	Alaska	San Fernando Island, NE Side	KF949308	MSB 221540
USA	Alaska	Cleveland Pen., 27 mi NNW Ketchikan	KF949309	UAM 20582
USA	Alaska	Etolin Island, Anita Bay	KF949310	UAM 20665
USA	Alaska	Kupreanof Island	KF949311	UAM 20945
USA	Alaska	Kupreanof Island	KF949312	UAM 20948
USA	Alaska	Noyes Island, Kelly Cove	KF949313	UAM 23655
USA	Alaska	Dall Island, Essowah Lakes	KF949314	UAM 23732
USA	Alaska	Union Bay, N shore at mouth	KF949315	UAM 23774
USA	Alaska	Revillagigedo Island, Orchard Lake	KF949316	UAM 23956
USA	Alaska	Suemez Island, Port Refugio	KF949317	UAM 23992
USA	Alaska	Baker Island, Port San Antonio	KF949318	UAM 30874
USA	Alaska	No specific locality recorded	KF949319	UAM 31103
USA	Alaska	10 km E, 9 km S Klukwan	KF949320	UAM 31107
USA	Alaska	Lulu Island	KF949321	UAM 42580
USA	Alaska	Lulu Island	KF949322	UAM 42581
USA	Alaska	Excursion Inlet, W side	KF949323	UAM 42939
USA	Alaska	Kuiu Island, Affleck Canal	KF949324	UAM 43431
USA	Alaska	Admiralty Island, W Gambier Bay	KF949325	UAM 44886
USA	Alaska	Admiralty Island, W Gambier Bay	KF949326	UAM 44888
USA	Alaska	Dyea, mouth W branch Taiya R	KF949328	UAM 76823
USA	Alaska	Prince of Wales Island, Turn Creek, El	KF949329	UAM 74970
USA	Alaska	Prince of Wales Island, Turn Creek, El	KF949330	UAM 74972
USA	Alaska	Zarembo Island, Saint John Harbor	KF949355	UAM 20619
USA	Alaska	Foggy Bay, Kirk Point	KF950008	UAM 23425

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Alaska	Mary Island, Customhouse Cove	KF950009	UAM 23437
USA	Alaska	Mary Island, Customhouse Cove	KF950010	UAM 23438
USA	Alaska	10 km E, 9 km S Klukwan	KF950011	UAM 31104
USA	Alaska	3.9 mi Haines Hwy/WNW of Haines	KF950012	UAM 48129
USA	Alaska	Prince of Wales Island, Ruth Cutoff	KF950013	UAM 49643
USA	Alaska	Haines, Chilkoot Lk Pk	KF950014	UAM 23667
USA	Alaska	Lulu Island	KF950015	UAM 43024
USA	Alaska	Union Bay, N shore at mouth	KF950016	UAM 23775
USA	Alaska	Kuiu Island, Rocky Pass, 1.5 km S. Sum.	KF950017	MSB 148973
USA	Alaska	Wrangell Island, Wrangell Ranger District	KF950018	MSB 149212
USA	Alaska	Zarembo Island, Saint John Harbor	KF950019	UAM 20620
USA	Alaska	Etolin Island, Anita Bay	KF950020	UAM 20662
USA	Alaska	Etolin Island, Anita Bay	KF950021	UAM 20664
USA	Alaska	Noyes Island, Kelly Cove	KF950022	UAM 23657
USA	Alaska	Noyes Island, Kelly Cove	KF950023	UAM 23658
USA	Alaska	Dall Island, Essowah Lakes	KF950024	UAM 23730
USA	Alaska	Union Bay, N shore at mouth	KF950025	UAM 23771
USA	Alaska	Union Bay, N shore at mouth	KF950026	UAM 23773
USA	Alaska	Revillagigedo Island, Ward Lake, Grassy	KF950027	UAM 30343
USA	Alaska	Kupreanof Island	KF950028	UAM 30590
USA	Alaska	Baranof Island, Plotnikof Lake	KF950029	UAM 30819
USA	Alaska	Baker Island, Port San Antonio	KF950030	UAM 30873
USA	Alaska	Klehini R, 5 km W Klukwan	KF950031	UAM 31105
USA	Alaska	10 km E, 9 km S Klukwan	KF950032	UAM 31106
USA	Alaska	Admiralty Island	KF950033	UAM 35318
USA	Alaska	Lulu Island	KF950034	UAM 42578
USA	Alaska	Lulu Island	KF950035	UAM 42579
USA	Alaska	Zarembo Island	KF950036	UAM 43469
USA	Alaska	Admiralty Island, W Gambier Bay	KF950037	UAM 44887
USA	Alaska	Dyea, mouth W branch Taiya R	KF950038	UAM 50436
USA	Alaska	Dyea, mouth W branch Taiya R	KF950039	UAM 52310
USA	Alaska	10 km E, 9 km S Klukwan	KF950040	UAM 60272
USA	Alaska	8.5 mi SE Goldbelt logging camp, Hobart	KF950041	UAM 74125
USA	Alaska	8.5 mi SE Goldbelt logging camp, Hobart	KF950042	UAM 74128
USA	Alaska	8.5 mi SE Goldbelt logging camp, Hobart	KF950043	UAM 74131
USA	Alaska	Dall Island, Essowah Lakes	KF950044	UAM 76238
USA	Alaska	Baker Island, Port San Antonio	KF950045	UAM 76353
USA	Alaska	Dyea, mouth W branch Taiya R	KF950046	UAM 76821
USA	Alaska	Dyea, mouth W branch Taiya R	KF950047	UAM 76822
USA	Alaska	Mitkof Island, 0.75 mi S Blind Slough	KF950048	UAM 23106

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Alaska	Mitkof Island, 0.75 mi S Blind Slough	KF950049	UAM 23107
USA	Alaska	Port Alice, at dump	KF950050	UAM 23487
USA	Alaska	mouth of Unuk River	KF950051	UAM 23490
USA	Alaska	Haines, Chilkoot Lk Pk	KF950052	UAM 23665
USA	Alaska	Heceta Island, Port Alice, Mint Lake	KF950053	UAM 23829
USA	Alaska	Heceta Island, Port Alice, Mint Lake	KF950054	UAM 23830
USA	Alaska	Heceta Island, Port Alice, Mint Lake	KF950055	UAM 23834
USA	Alaska	Baranof Island, Plotnikof Lake	KF950056	UAM 30821
USA	Alaska	Baranof Island, Plotnikof Lake	KF950057	UAM 30822
USA	Alaska	Warren Island, Warren cove	KF950058	UAM 31725
USA	Alaska	Etolin Island, Anita Bay	KF950059	UAM 41652
USA	Alaska	Forrester Island, Eagle Harbor	KF950060	UAM 42788
USA	Alaska	Forrester Island, Eagle Harbor	KF950061	UAM 42790
USA	Alaska	Forrester Island, Eagle Harbor	KF950062	UAM 42795
USA	Alaska	San Fernando Island	KF950063	UAM 42800
USA	Alaska	San Fernando Island	KF950064	UAM 42804
USA	Alaska	San Fernando Island	KF950065	UAM 42836
USA	Alaska	NE side of Coronation Island, Spanish	KF950066	UAM 42924
USA	Alaska	Kosciusko Island, 2 mi NE Edna Bay	KF950067	UAM 49631
USA	Alaska	Wrangell Island, Fools Creek	KF950068	UAM 69668
USA	Alaska	Wrangell Island, Fools Creek	KF950069	UAM 69673
USA	Alaska	Gravina Island, Phocena Bay	KF950070	UAM 70144
USA	Alaska	Gravina Island, Phocena Bay	KF950071	UAM 70150
USA	Alaska	Gravina Island, Phocena Bay	KF950072	UAM 70152
USA	Alaska	Dall Island, North Bay	KF950073	UAM 73711
USA	Alaska	Dall Island, Tlevak Narrows	KF950074	UAM 73829
USA	Alaska	Chichagof Island, Salt Lake Bay	KF950075	UAM 76385
USA	Alaska	Revillagigedo Island, Ella Bay	KF950129	UAM 23442
USA	Alaska	Noyes Island, Kelly Cove	KF950130	UAM 23656
USA	Alaska	Kirk Point	KF950131	UAM 30391
USA	Alaska	Turner Lake	KF950132	UAM 50754
USA	Alaska	Chichagof Island, Salt Lake Bay	KF950133	UAM 50932
USA	Alaska	Revillagigedo Island, Ella Bay	KF964334	UAM 23449
USA	Washington	Gifford Pinchot National Forest, Little	AY184570	UWBM 73844
USA	Washington	Roger's Lake; off FS# 37, 1.5 mi FS# 39	AY184595	UWBM 73638
USA	Washington	24 mi (by road) NW Winthrop, Hwy 20	DQ385716	MSB 61426
USA	Washington	Olympic National Park; Elwha Valley	KF949331	UWBM 74932
USA	Washington	Olympic National Park; Elwha Valley	KF949352	UWBM 74954

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
		Peromyscus labecula		
Mexico	Chihuahua	2.2 mi N, 1 mi W San Juanito	DQ385717	MSB 58334
Mexico	Durango	Hacienda Coyotes	AY322508	TTU 81622
Mexico	Veracruz	Perote	MH299892	TTU 104953
Mexico	Veracruz	Perote	MH299893	TTU 104954
Mexico	Zacatecas	Concepcion del Oro	MH299894	TTU 45159
USA	New Mexico	Animas Valley, Clanton Draw Tanks	DQ385718	MSB 46243
USA	New Mexico	18 mi N Rodeo	DQ385719	MSB 51140
USA	New Mexico	1 mi S, 6.4 mi W Animas, Antelope Pass	DQ385720	MSB 51133
USA	New Mexico	1 mi S, 6.4 mi W Animas, Antelope Pass	DQ385721	MSB 51132
USA	New Mexico	6.2 mi NW of Timberon on Road 537	DQ385722	MSB 75513
USA	Texas	Mentone	MN124382	TTU 45582
USA	Texas	Sierra Blanca	MN124381	TTU 53103
		Peromyscus maniculatus		
Canada	Labrador	Herbon	DQ385809	OSM 722
Canada	Labrador	Herbon	DQ385810	OSM 723
Canada	Labrador	Herbon	DQ385811	OSM 726
Canada	Labrador	Herbon	DQ385812	OSM 725
Canada	Labrador	Herbon	DQ385813	OSM 724
Canada	Labrador	Nain	DQ385814	OSM 735
Canada	Labrador	Nain	DQ385815	OSM 737
Canada	Manitoba	8 km S, 14 km E Flin Flon, Scotty Lake	DQ385723	MSB 55764
Canada	Manitoba	8 km S, 14 km E Flin Flon	DQ385724	MSB 55765
Canada	Manitoba	12 km S, 15 km E Flin Flon, HWY 10	DQ385725	MSB 55767
Canada	Manitoba	1 mi N, 5 mi E Marchand, Sandilands	DQ385726	MSB 53321
Canada	Manitoba	0.5 mi N, 5 mi E Marchand, Sandilands	DQ385727	MSB 53325
Canada	Manitoba	vic. Thompson	DQ385728	OSM 493
Canada	Manitoba	vic. Thompson	DQ385729	OSM 490
Canada	Manitoba	vic. Thompson	DQ385730	OSM 492
Canada	Manitoba	Wallace Lake, Taiga Biological Station	DQ385731	OSM 430
Canada	Manitoba	Wallace Lake, Taiga Biological Station	DQ385732	OSM 439
Canada	Manitoba	Wallace Lake, Taiga Biological Station	DQ385733	OSM 441
Canada	Manitoba	18 km west and 4 km north of Gillam	MG602680	MSB 285147
Canada	Manitoba	18 km west and 4 km north of Gillam	MG602681	MSB 285143
Canada	Ontario	vic. Thunder Bay	DQ385734	CM 109530
Canada	Ontario	vic. Thunder Bay	DQ385735	CM 109534
Canada	Ontario	Hastings, 0.5 mi N, 3 mi W Gilmour	DQ385770	MSB 53341
Canada	Ontario	Elliot Lake	DQ385771	OSM 626
Canada	Ontario	Elliot Lake	DQ385772	OSM 622
Canada	Ontario	Elliot Lake	DQ385773	OSM 625

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
Canada	Ontario	Algonquin Provincial Park	DQ385774	OSM 216
Canada	Ontario	Algonquin Provincial Park	DQ385775	OSM 221
Canada	Ontario	Algonquin Provincial Park	DQ385776	OSM 222
Canada	Ontario	Bruce Peninsula	DQ385777	OSM 294
Canada	Ontario	Bruce Peninsula	DQ385778	OSM 296
Canada	Ontario	Bruce Peninsula	DQ385779	OSM 297
Canada	Ontario	Ivanhoe Lake	DQ385780	OSM 585
Canada	Ontario	Ivanhoe Lake	DQ385781	OSM 586
Canada	Ontario	Ivanhoe Lake	DQ385782	OSM 587
Canada	Quebec	Gaspe Peninsula	DQ385749	CM 109316
Canada	Quebec	Gaspe Peninsula	DQ385750	CM109317
Canada	Quebec	Gaspe Peninsula	DQ385751	CM 109318
Canada	Quebec	Gaspe Peninsula	DQ385752	CM 109328
Canada	Quebec	Gaspe Peninsula	DQ385753	CM 109319
Canada	Quebec	135 km N Baie Comeau	DQ385783	OSM 78
Canada	Quebec	136 km N Baie Comeau	DQ385784	OSM 79
Canada	Quebec	137 km N Baie Comeau	DQ385785	OSM 811
Canada	Quebec	Zenon	DQ385786	OSM 843
Canada	Quebec	Zenon	DQ385787	OSM 845
Canada	Quebec	Zenon	DQ385788	OSM 846
Canada	Quebec	W of Mistassini Lake	DQ385789	OSM 1182
Canada	Quebec	W of Mistassini Lake	DQ385790	OSM 1183
Canada	Quebec	W of Mistassini Lake	DQ385791	OSM 1185
Canada	Quebec	Transtaiga Hwy (near James Bay)	DQ385792	OSM 917
Canada	Quebec	Transtaiga Hwy (near James Bay)	DQ385793	OSM 918
Canada	Quebec	Transtaiga Hwy (near James Bay)	DQ385794	OSM 919
Canada	Quebec	Sept-Iles	DQ385795	CM 109563
Canada	Quebec	Sept-Iles	DQ385796	CM 109564
Canada	Quebec	Sept-Iles	DQ385797	CM 109565
Canada	Quebec	Sept-Iles	DQ385798	CM 10956
Canada	Quebec	Sept-Iles	DQ385799	CM 109569
Canada	Quebec	Hebertville, Lac Kenogami	DQ385800	CM 109407
Canada	Quebec	Hebertville, Lac Kenogami	DQ385801	CM 109408
Canada	Quebec	Hebertville, Lac Kenogami	DQ385802	CM 109409
Canada	Quebec	Hebertville, Lac Kenogami	DQ385803	CM 109410
Canada	Quebec	Hebertville, Lac Kenogami	DQ385804	CM 109411
Canada	Quebec	E of Mistassini Lake	DQ385805	CM 109499
Canada	Quebec	E of Mistassini Lake	DQ385806	CM 109538
Canada	Quebec	E of Mistassini Lake	DQ385807	CM 109540
Canada	Quebec	E of Mistassini Lake	DQ385808	CM 109541

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Maine	vic. Orono	DQ385754	CM 109330
USA	Maine	vic. Orono	DQ385755	CM 109334
USA	Maine	vic. Orono	DQ385756	CM 109335
USA	Michigan	vic. Gaylord	DQ385821	SP 3035
USA	Michigan	vic. Gaylord	DQ385822	SP 3030
USA	Michigan	vic. Gaylord	DQ385823	SP 3029
USA	Michigan	St. Ignace (Upper Peninsula)	DQ385824	CM 109595
USA	Michigan	St. Ignace (Upper Peninsula)	DQ385825	CM 109419
USA	Michigan	St. Ignace (Upper Peninsula)	DQ385826	CM 109420
USA	Michigan	St. Ignace (Upper Peninsula)	DQ385827	CM 109441
USA	Minnesota	13 km W Remer	DQ385736	CM 109605
USA	Minnesota	13 km W Remer	DQ385737	CM 109438
USA	Minnesota	13 km W Remer	DQ385738	CM 109440
USA	Minnesota	13 km W Remer	DQ385739	CM 109604
USA	Minnesota	SE intersection Forest Rds 165 and 339	MN124380	TTU 57149
USA	New York	Mongaup Pond (in Catskills)	DQ385740	OSM 680
USA	New York	Mongaup Pond (in Catskills)	DQ385741	OSM 681
USA	New York	Mongaup Pond (in Catskills)	DQ385742	OSM 683
USA	New York	17 km W Salamanca	DQ385743	OSM 350
USA	New York	18 km W Salamanca	DQ385744	OSM 354
USA	New York	21 km W Salamanca	DQ385745	OSM 351
USA	New York	vic. Chazy	DQ385746	SP 9171
USA	New York	vic. Chazy	DQ385747	SP 9172
USA	New York	vic. Chazy	DQ385748	SP 9173
USA	Pennsylvania	8.1km W, 3.8km N Salisbury	DQ385762	CM 109276
USA	Pennsylvania	8.1km W, 3.8km N Salisbury	DQ385763	CM 109278
USA	Pennsylvania	8.1km W, 3.8km N Salisbury	DQ385764	CM 109546
USA	Pennsylvania	8.1km W, 3.8km N Salisbury	DQ385765	CM 109547
USA	Pennsylvania	8.1km W, 3.8km N Salisbury	DQ385766	CM109548
USA	Tennessee	Unicoi Co. (only locality information)	DQ385767	CM 106498
USA	Tennessee	Unicoi Co. (only locality information)	DQ385768	CM 106499
USA	Tennessee	Unicoi Co. (only locality information)	DQ385769	CM 106500
USA	Tennessee	Newfoundland Gap RD Loop	DQ385816	MSB 71956
USA	Tennessee	Newfoundland Gap RD Loop	DQ385817	MSB 71957
USA	Tennessee	Newfoundland Gap RD Loop	DQ385818	MSB 71965
USA	Tennessee	Unicoi Co. (only locality information)	DQ385819	CM 106505
USA	Tennessee	Unicoi Co. (only locality information)	DQ385820	CM 106503
USA	Virginia	Shenandoah National Park	DQ385757	MSB 74561
USA	Virginia	Shenandoah National Park	DQ385758	MSB 74568
USA	Virginia	Shenandoah National Park	DQ385759	MSB 74926

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Virginia	Shenandoah National Park	DQ385760	MSB 74932
USA	Virginia	Shenandoah National Park	DQ385761	MSB 74936
		Peromyscus melanotis		
Mexico	Chihuahua	2.2 mi N, 1 mi W San Juanito	DQ385627	NK 7395L1
Mexico	Durango	12 km E Ojitos	AF155398	CRD 2025
Mexico	Mexico DC	17.5 km S, 7.0 km W Toluca	DQ385626	MSB 12187
Mexico	Veracruz	6.7 km NE, 14 km SE Perote	KY064167	TTU 105030
USA	Arizona	Cochise Co. (only locality information)	EU574700	JFS 47
USA	Arizona	Cochise Co. (only locality information)	EU574701	JFS 5
		Peromyscus polionotus		
USA	Florida	J Archbold Biological Station	F322885	CLP 1113
USA	Florida	Archbold Biological Station	JF322886	CLP 1114
USA	Florida	Archbold Biological Station	JF322887	CLP 1116
USA	Florida	Ocala National Forest	JF322888	CLP 1117
USA	Florida	Ocala National Forest	JF322889	CLP 1118
USA	Florida	Ocala National Forest	JF322890	CLP 1119
USA	Florida	Ocala National Forest	JF322891	CLP 1120
USA	Florida	Ocala National Forest	JF322892	CLP 1121
USA	Florida	Suwannee Ridge WEA	JF322893	CLP 1122
USA	Florida	Suwannee Ridge WEA	F322894	CLP 1123
USA	Florida	Suwannee Ridge WEA	JF322895	CLP 1124
USA	Florida	Suwannee Ridge WEA	JF322896	CLP 1125
USA	Florida	Anastasia State Park	JF322897	CLP 1126
		Peromyscus sejugis		
Mexico	Baja California Sur	Isla Santa Cruz	MF589856	CIB 667
		Peromyscus sonoriensis		
Canada	Alberta	Kanaanaskis Field Station	KF949166	MSB 156182
Canada	Alberta	Kanaanaskis Field Station	KF949201	MSB 156150
Canada	Alberta	Kanaanaskis Field Station	KF949202	MSB 156183
Canada	British Columbia	Vancouver Island, village of Ucluelet	DQ385698	MSB 83399
Canada	British Columbia	Vancouver Island, village of Ucluelet	DQ385699	MSB 83409
Canada	British Columbia	Vancouver Island, village of Ucluelet	DQ385700	MSB 83419
Canada	British Columbia	Vancouver Island, village of Ucluelet	DQ385702	MSB 83417
Canada	British Columbia	Nancy Green Summit	KF949167	MSB 156370
Canada	British Columbia	Nancy Green Summit	KF949168	MSB 156589
Canada	British Columbia	1 km W Elko, Kikoman Creek, Prov. Park	KF949196	MSB 56704
Canada	British Columbia	1 km W Elko, Kikoman Creek, Prov. Park	KF949197	MSB 56705
Canada	British Columbia	1 km W Elko, Kikoman Creek, Prov. Park	KF949198	MSB 56706
Canada	British Columbia	Nancy Green Summit	KF949203	MSB 156364
Canada	British Columbia	Nancy Green Summit	KF949204	MSB 156365

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
Canada	British Columbia	Atlin	KF949208	UAM 52689
Canada	British Columbia	Atlin	KF949209	UAM 35341
Canada	British Columbia	Atlin	KF949210	UAM 52696
Canada	British Columbia	Atlin	KF949211	UAM 52699
Canada	British Columbia	Atlin	KF949212	UAM 52700
Canada	British Columbia	Atlin	KF949213	UAM 52967
Canada	British Columbia	Atlin	KF949214	UAM 52690
Canada	British Columbia	Atlin	KF949215	UAM 52691
Canada	British Columbia	Atlin	KF949216	UAM 52692
Canada	British Columbia	Atlin	KF949217	UAM 52693
Canada	British Columbia	S Side Stikine River	KF949218	MSB 158026
Canada	British Columbia	S Side Stikine River	KF949219	MSB 158027
Canada	British Columbia	S Side Stikine River	KF949220	MSB 158207
Canada	British Columbia	S Side Stikine River	KF949236	MSB 158235
Canada	British Columbia	Cassiar Highway (Hwy 37), Rescue Creek	KF949240	MSB 155835
Canada	British Columbia	Cassiar Highway (Hwy 37), Rescue Creek	KF949241	MSB 155850
Canada	British Columbia	Atlin	KF949247	UAM 52701
Canada	British Columbia	4.5mi S of Dease Lake	KF949248	MSB 199034
Canada	British Columbia	Atlin	KF949250	UAM 35335
Canada	British Columbia	Atlin	KF949251	UAM 35336
Canada	British Columbia	Cassiar Highway (Hwy 37), Todagin Riv.	KF949252	MSB 147166
Canada	British Columbia	Atlin	KF949266	UAM 35337
Canada	Northwest Terr.	Fort Smith, Fox Hole Road	KF949170	UAM 77795
Canada	Yukon - South	Agay Mene Territorial Park	KF949224	MSB 194099
Canada	Yukon Territory	Agay Mene Territorial Park	KF949221	MSB 194065
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949222	MSB 194085
Canada	Yukon Territory	Agay Mene Territorial Park	KF949223	MSB 194097
Canada	Yukon Territory	Agay Mene Territorial Park	KF949225	MSB 194102
Canada	Yukon Territory	Agay Mene Territorial Park	KF949226	MSB 194103
Canada	Yukon Territory	Agay Mene Territorial Park	KF949227	MSB 194104
Canada	Yukon Territory	Agay Mene Territorial Park	KF949228	MSB 194105
Canada	Yukon Territory	Agay Mene Territorial Park	KF949229	MSB 194113
Canada	Yukon Territory	Agay Mene Territorial Park	KF949230	MSB 194114
Canada	Yukon Territory	71 km E Watson Lake	KF949231	MSB 194127
Canada	Yukon Territory	71 km E Watson Lake	KF949232	MSB 194129
Canada	Yukon Territory	71 km E Watson Lake	KF949233	MSB 194130
Canada	Yukon Territory	Agay Mene Territorial Park	KF949234	MSB 194166
Canada	Yukon Territory	Fox Creek on Hwy 2	KF949235	MSB 144237
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949237	MSB 144139
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949238	MSB 144142

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
Canada	Yukon Territory	Canol Highway; Rose River Crossing #1	KF949239	MSB 149188
Canada	Yukon Territory	Fox Creek on Hwy 2	KF949242	MSB 144238
Canada	Yukon Territory	Fox Creek on Hwy 2	KF949243	MSB 144239
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949244	MSB 144240
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949245	MSB 144151
Canada	Yukon Territory	Agay Mene Territorial Park	KF949246	MSB 194080
Canada	Yukon Territory	1 mi S Lake Laberge Campgrd.on Hwy 2	KF949249	MSB 144409
Canada	Yukon Territory	LaBiche River; 40 km ESE of Fort Liard	KF949253	MSB 144150
Canada	Yukon Territory	Garden Creek; 7 km NE of Watson Lake	KF949254	MSB 144364
Canada	Yukon Territory	Garden Creek; 7 km NE of Watson Lake	KF949255	MSB 144387
Canada	Yukon Territory	Garden Creek; 7 km NE of Watson Lake	KF949262	MSB 144366
USA	Alaska	Tiekel River	FJ415092	MSB 192746
USA	Alaska	Tiekel River	FJ415093	MSB 192747
USA	Alaska	Tiekel River	FJ415094	MSB192748
USA	Alaska	Tiekel River	FJ415095	MSB 192749
USA	Arizona	Petrified Forest National Park	KF949161	MSB 122918
USA	California	3.8 mi S, 2.7 mi E Trinidad, T7N, R1E	DQ385703	MSB 43630
USA	California	3.8 mi S, 2.7 mi E Trinidad, T7N, R1E	DQ385704	MSB 43631
USA	California	3.8 mi S, 2.7 mi E Trinidad, T7N, R1E	DQ385705	MSB 43633
USA	California	Reeve's Ranch, 0.7 mi WNW La Grange	EF666146	MVZ 207842
USA	California	upper Lyell Canyon, Yosemite NP	EF666155	MVZ 202234
USA	California	upper Lyell Canyon, Yosemite NP	EF666161	MVZ 202250
USA	California	upper Lyell Canyon, Yosemite NP	EF666162	MVZ 202252
USA	California	upper Lyell Canyon, Yosemite NP	EF666163	MVZ 202258
USA	California	Yosemite National Park	EF666167	MVZ 208026
USA	California	Yosemite National Park	EF666178	MVZ 208098
USA	California	Barcroft Research Station	EF666179	WM 2
USA	California	Barcroft Research Station	EF666182	WM 7
USA	California	5.2 km S Olema	EU006766	MVZ 191735
USA	California	Point Reyes National Seashore	EU006767	MVZ 196031
USA	California	Point Reyes National Seashore	EU006768	MVZ 196032
USA	California	Point Reyes National Seashore	EU006769	MVZ 196029
USA	California	Point Reyes National Seashore	EU006770	MVZ 196028
USA	California	Point Reyes National Seashore	EU006771	MVZ 196030
USA	California	Fox Creek Lodge, Angelo Coast Reserve	EU006772	MVZ 199143
USA	Colorado	40 40'N, 104 22'W	DQ385690	MSB 74662
USA	Colorado	40 40'N, 104 22'W	DQ385691	MSB 74663
USA	Colorado	40 40'N, 104 22'W	DQ385692	MSB 74667
USA	Colorado	40 40'N, 104 22'W	DQ385693	MSB 74669
USA	Colorado	Yuma Co. (only locality information)	EF666212	JFS 107

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Colorado	Yuma Co. (only locality information)	EF666213	JFS 114
USA	Colorado	Yuma Co. (only locality information)	EF666214	JFS 117
USA	Colorado	Yuma Co. (only locality information)	EF666215	JFS 122
USA	Colorado	Yuma Co. (only locality information)	EF666216	JFS 123
USA	Colorado	Yuma Co. (only locality information)	EF666217	JFS 124
USA	Colorado	Yuma Co. (only locality information)	EF666218	JFS 132
USA	Colorado	Yuma Co. (only locality information)	EF666219	JFS 134
USA	Colorado	Yuma Co. (only locality information)	EF666220	JFS 135
USA	Colorado	Yuma Co. (only locality information)	EF666221	JFS 137
USA	Colorado	Yuma Co. (only locality information)	EF666222	JFS 140
USA	Colorado	Yuma Co. (only locality information)	EF666223	JFS 136
USA	Colorado	Yuma Co. (only locality information)	EF666224	JFS 143
USA	Colorado	Yuma Co. (only locality information)	EF666225	JFS 141
USA	Colorado	Yuma Co. (only locality information)	EF666226	JFS 142
USA	Colorado	Clear Creek Co. (only locality info.)	EF666227	JFS 70
USA	Colorado	Clear Creek Co. (only locality info.)	EF666228	JFS 71
USA	Colorado	Clear Creek Co. (only locality info.)	EF666229	JFS 73
USA	Colorado	Clear Creek Co. (only locality info.)	EF666230	JFS 74
USA	Colorado	Clear Creek Co. (only locality info.)	EF666231	JFS 76
USA	Colorado	Clear Creek Co. (only locality info.)	EF666232	JFS 80
USA	Colorado	Clear Creek Co. (only locality info.)	EF666233	JFS 81
USA	Colorado	Clear Creek Co. (only locality info.)	EF666234	JFS 82
USA	Colorado	Clear Creek Co. (only locality info.)	EF666235	JFS 87 Clear
USA	Colorado	Clear Creek Co. (only locality info.)	EF666236	JFS 88 Clear
USA	Colorado	Clear Creek Co. (only locality info.)	EF666237	JFS 95 Clear
USA	Colorado	Clear Creek Co. (only locality info.)	EF666238	JFS 97 Clear
USA	Colorado	Clear Creek Co. (only locality info.)	EF666240	JFS 100
USA	Colorado	Clear Creek Co. (only locality info.)	EF666241	JFS 106
USA	Colorado	Weld Co. (only locality information)	EF666244	MSB 74669
USA	Colorado	Weld Co. (only locality information)	EF666245	MSB 74664
USA	Colorado	Weld Co. (only locality information)	EF666246	MSB 74665
USA	Colorado	Weld Co. (only locality information)	EF666247	MSB 74666
USA	Colorado	Weld Co. (only locality information)	EF666249	MSB 74670
USA	Colorado	Weld Co. (only locality information)	EF666250	MSB 74673
USA	Colorado	Weld Co. (only locality information)	EF666251	NK 56092
USA	Colorado	Weld Co. (only locality information)	EF666252	MSB 74580
USA	Colorado	Weld Co. (only locality information)	EF666253	MSB 74581
USA	Colorado	Boulder Co. (only locality information)	EF666255	JFS 20
USA	Colorado	Boulder Co. (only locality information)	EF666256	JFS 26
USA	Colorado	Boulder Co. (only locality information)	EF666257	JFS 27

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Colorado	Boulder Co. (only locality information)	EF666258	JFS 28
USA	Colorado	Boulder Co. (only locality information)	EF666259	JFS 7
USA	Colorado	Boulder Co. (only locality information)	EF666260	JFS 8
USA	Colorado	Boulder Co. (only locality information)	EF666261	JFS 9
USA	Colorado	Boulder Co. (only locality information)	EF666262	JFS 10
USA	Colorado	Boulder Co. (only locality information)	EF666263	JFS 11
USA	Colorado	Boulder Co. (only locality information)	EF666264	JFS 12
USA	Colorado	Boulder Co. (only locality information)	EF666265	JFS 13
USA	Colorado	Boulder Co. (only locality information)	EF666266	JFS 14
USA	Colorado	Boulder Co. (only locality information)	EF666267	JFS 15
USA	Colorado	Boulder Co. (only locality information)	EF666268	JFS 16
USA	Colorado	Boulder Co. (only locality information)	EF666269	JFS 17
USA	Colorado	Boulder Co. (only locality information)	EF666270	JFS 18
USA	Colorado	Boulder Co. (only locality information)	EF666271	JFS 19
USA	Colorado	Boulder Co. (only locality information)	EF666272	JFS 21
USA	Colorado	Boulder Co. (only locality information)	EF666273	JFS 22
USA	Colorado	Boulder Co. (only locality information)	EF666274	JFS 23
USA	Colorado	Boulder Co. (only locality information)	EF666275	JFS 24
USA	Colorado	Boulder Co. (only locality information)	EF666276	JFS 25
USA	Colorado	Boulder Co. (only locality information)	EF666277	JFS 29
USA	Idaho	2 mi W, 8 mi S of Snake River Birds of	DQ385672	MSB 74885
USA	Idaho	2 mi W, 8 mi S of Snake River Birds of	DQ385673	MSB 74886
USA	Idaho	2 mi W, 8 mi S of Snake River Birds of	DQ385674	MSB 74894
USA	Idaho	2 mi W, 8 mi S of Snake River Birds of	DQ385675	MSB 74897
USA	Idaho	Near Atomic City	EF100717	MSB 151508
USA	Idaho	Near Atomic City	EF100718	MSB 151510
USA	Idaho	Near Atomic City	EF100720	MSB 151518
USA	Idaho	City of Rocks National Reserve	FJ800584	UWBM 79662
USA	Idaho	Near Atomic City	KF949172	MSB 151511
USA	Iowa	Iowa Army Ammunition Plant	DQ385633	MSB 84837
USA	Iowa	Iowa Army Ammunition Plant	DQ385634	MSB 84833
USA	Iowa	Iowa Army Ammunition Plant	DQ385635	MSB 84845
USA	Iowa	Iowa Army Ammunition Plant	DQ385636	MSB 84847
USA	Iowa	Iowa Army Ammunition Plant	DQ385637	MSB 84841
USA	Kansas	Fort Larned National Historic Site	DQ385638	MSB 73952
USA	Kansas	Fort Larned National Historic Site	DQ385639	MSB 73954
USA	Kansas	Fort Larned National Historic Site	DQ385640	MSB 73957
USA	Kansas	Fort Larned National Historic Site	DQ385641	MSB 73960
USA	Kansas	Fort Larned National Historic Site	DQ385642	MSB 73966
USA	Kansas	Fort Larned National Historic Site	EF666197	MSB 73948

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Kansas	Fort Larned National Historic Site	EF666199	MSB 73953
USA	Kansas	Fort Larned National Historic Site	EF666200	MSB 73954
USA	Kansas	Fort Larned National Historic Site	EF666201	MSB 73955
USA	Kansas	Fort Larned National Historic Site	EF666202	MSB 73957
USA	Kansas	Fort Larned National Historic Site	EF666203	MSB 73958
USA	Kansas	Fort Larned National Historic Site	EF666204	MSB 73961
USA	Kansas	Fort Larned National Historic Site	EF666205	MSB 73966
USA	Kansas	Fort Larned National Historic Site	EF666206	MSB 73967
USA	Kansas	Fort Larned National Historic Site	EF666207	MSB 73968
USA	Kansas	Fort Larned National Historic Site	EF666208	NK 53269
USA	Kansas	Fort Larned National Historic Site	EF666209	MSB 73972
USA	Kansas	Fort Larned National Historic Site	EF666210	NK 53277
USA	Michigan	Isle Royale	DQ385643	OSM 869
USA	Michigan	Isle Royale	DQ385644	OSM 870
USA	Michigan	Isle Royale	DQ385645	OSM 871
USA	Missouri	5.8 mi SE Ava	MN124386	TTU 62040
USA	Montana	9 mi S Bozeman, Hyalite Creek	DQ385676	MSB 56716
USA	Montana	9 mi S Bozeman, Hyalite Creek	DQ385677	MSB 56718
USA	Montana	9 mi S Bozeman, Hyalite Creek	DQ385678	MSB 56717
USA	Montana	9 mi S Bozeman, Hyalite Creek	DQ385679	MSB 56719
USA	New Mexico	Canon Air Force Base	DQ385628	MSB 75831
USA	New Mexico	Canon Air Force Base	DQ385629	MSB 75832
USA	New Mexico	Canon Air Force Base	DQ385630	MSB 75835
USA	New Mexico	Canon Air Force Base	DQ385631	MSB 75844
USA	New Mexico	Canon Air Force Base	DQ385632	MSB 76102
USA	New Mexico	9mi S, 5 mi E of Magdalena	DQ385646	MSB 69326
USA	New Mexico	9mi S, 5 mi E of Magdalena	DQ385647	MSB 69322
USA	New Mexico	9mi S, 5 mi E of Magdalena	DQ385648	MSB 69324
USA	New Mexico	9mi S, 5 mi E of Magdalena	DQ385649	MSB 69325
USA	New Mexico	9mi S, 5 mi E of Magdalena	DQ385650	MSB 69323
USA	New Mexico	Negrito Airfield Base Camp	DQ385651	MSB 82183
USA	New Mexico	Gilsons Cienega Marsh	DQ385652	MSB 89387
USA	New Mexico	3 mi E, 3 mi S Sedillo, Zuniga's Kitchen	DQ385653	MSB 77901
USA	New Mexico	3 mi E, 3 mi S Sedillo, Zuniga's Kitchen	DQ385654	MSB 77903
USA	New Mexico	Cedar Crest Mountain Hostel, 3.5 mi N	DQ385655	MSB 72700
USA	New Mexico	Cedar Crest Mountain Hostel, 3.5 mi N	DQ385656	MSB 72697
USA	New Mexico	6.1mi N of Gila	DQ385657	NK 102839
USA	New Mexico	4.8 mi NW of Timberon on RD 537	DQ385658	MSB 75491
USA	New Mexico	5.2 mi NW of Timberon on RD 537	DQ385659	MSB 75495
USA	New Mexico	5.2 mi NW of Timberon on RD 537	DQ385660	MSB 75499

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	New Mexico	Holloman Air Force Base, T15, S R8 E	DQ385661	MSB 89198
USA	New Mexico	Tularosa Mountains	DQ385662	MSB 89460
USA	New Mexico	4.8 mi NW of Timberon on RD 537	DQ385663	MSB 75492
USA	New Mexico	6.2 mi NW of Timberon on RD 537	DQ385664	MSB 75505
USA	New Mexico	6.2 mi NW of Timberon on RD 537	DQ385665	MSB 75509
USA	New Mexico	6.2 mi NW of Timberon on RD 537	DQ385666	MSB 75511
USA	New Mexico	57 km S Farmington	DQ385667	MSB 90205
USA	New Mexico	57 km S Farmington	DQ385668	MSB 90206
USA	New Mexico	57 km S Farmington	DQ385669	MSB 90216
USA	New Mexico	57 km S Farmington	DQ385670	MSB 90219
USA	New Mexico	57 km S Farmington	DQ385671	MSB 90220
USA	Nevada	Naval Air Station Fallon, 1300 m	DQ385680	MSB 74964
USA	Nevada	Naval Air Station Fallon, 1300 m	DQ385681	MSB 74970
USA	Nevada	Naval Air Station Fallon, 1300 m	DQ385682	MSB 74974
USA	Nevada	Naval Air Station Fallon, 1300 m	DQ385683	MSB 74983
USA	Nevada	White Pine Co. (only locality info.)	EF666185	EAR 3286
USA	Nevada	White Pine Co. (only locality info.)	EF666186	EAR 5078
USA	Nevada	White Pine Co. (only locality info.)	EF666187	EAR 5079
USA	Nevada	White Pine Co. (only locality info.)	EF666188	EAR 5147
USA	Nevada	White Pine Co. (only locality info.)	EF666189	EAR 5166
USA	Nevada	White Pine Co. (only locality info.)	EF666190	EAR 5167
USA	Nevada	White Pine Co. (only locality info.)	EF666191	EAR 5169
USA	Nevada	White Pine Co. (only locality info.)	EF666192	EAR 5170
USA	Nevada	White Pine Co. (only locality info.)	EF666193	EAR 5171
USA	Nevada	White Pine Co. (only locality info.)	EF666194	EAR 5173
USA	Nevada	White Pine Co. (only locality info.)	EF666195	EAR 5182
USA	Nevada	White Pine Co. (only locality info.)	EF666196	EAR 5185
USA	Oregon	T27S R3E Sec 2 W1/2	AY184697	UWBM 76586
USA	Oregon	Umatilla National Forest S of Hwy 244	AY184700	UWBM 75403
USA	Oregon	Dechutes National Forest ~0.5 mi	AY184701	UWBM 75420
USA	Oregon	Siuslaw National Forest Three River	AY184749	UWBM 75436
USA	Oregon	Ochoco National Forest; Ochoco Mts.	KF949191	MSB 155558
USA	Texas	5 mi S, 3 mi W Dimmitt	AY041199	TTU 55848
USA	Texas	3.6 mi S Wichita Falls	DQ000484	TTU 38739
USA	Texas	2 mi S, 5 mi E Tahoka	MN124385	TTU 77571
USA	Texas	Caprock Canyons State Park	MN124387	TTU 69199
USA	Utah	Lehi	AY859473	BYU 14073
USA	Utah	Camp William Wood Hollow Line 5	DQ385684	MSB 72067
USA	Utah	Camp William Wood Hollow Line 5	DQ385685	MSB 72070
USA	Utah	Camp William Wood Hollow Line 5	DQ385686	MSB 72103

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
USA	Utah	Camp William Wood Hollow Line 5	DQ385687	MSB 72119
USA	Utah	Camp William Wood Hollow Line 5	DQ385688	MSB 72135
USA	Utah	Salt Lake Co. (only locality information)	EF666254	Unvouchered
USA	Washington	Hwy 153, 8 road mi on FS#4010	AY184686	UWBM 73611
USA	Washington	Panjab Creek; T8N R41E Sec 5	AY184689	UWBM 73914
USA	Washington	Harvey Creek; T37N R44E Sec 2	AY184691	UWBM 73945
USA	Washington	Frenchman Coulee	AY184703	UWBM 72501
USA	Washington	Sugarloaf Peak Vicinity; T26N R18E	AY184705	UWBM 73790
USA	Washington	South Fork Taneum Creek, Wenatchee	AY184717	UWBM 73822
USA	Washington	Lake Chelan National Rec. Area	AY184733	UWBM 73774
USA	Washington	Simcoe Mountain, Monument Road	AY184739	UWBM 73836
USA	Washington	off FS# 37, 3 road mi on FS# 39; Freeze	AY184753	UWBM 73640
USA	Washington	W fork of Granite Creek; T37 R31 Sec 26	AY184754	UWBM 74052
USA	Washington	2 mi S, 0.5 mi W Roslyn, Cleelum River	DQ385689	MSB 43433
USA	Washington	Bainbridge Island, Naval Submarine Base	DQ385694	MSB 83495
USA	Washington	Naval Radio Station, Jim Creek	DQ385695	MSB 83456
USA	Washington	1 mi N, 5 mi W Greenwater	DQ385696	MSB 55699
USA	Washington	Fort Lewis, Youth Camp	DQ385697	MSB 86381
		Peromyscus sp.		
Canada	Yukon	Alaska Highway	KF949156	UAM 52705
Canada	Yukon	27.5 mi S Pelly Crossing on Hwy 2	KF949162	MSB 144216
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949163	MSB 144284
Canada	Yukon	North Fork of Klondike River on Hwy 5	KF949164	MSB 145572
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949165	MSB 149206
Canada	Yukon	35 km S Haines Junction	KF949169	MSB 240539
Canada	Yukon	27.5 mi S Pelly Crossing on Hwy 2	KF949171	MSB 144217
Canada	Yukon	35 km S Haines Junction	KF949173	MSB 240553
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949174	MSB 144263
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949175	MSB 144264
Canada	Yukon	North Fork of Klondike River on Hwy 5	KF949176	MSB 145250
Canada	Yukon	McQuesten River on Hwy 2	KF949177	MSB 145618
Canada	Yukon	McQuesten River on Hwy 2	KF949178	MSB 145637
Canada	Yukon	Dawson City	KF949179	MSB 145713
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949180	MSB 144265
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949181	MSB 149203
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949182	MSB 149204
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949183	MSB 149205
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949184	MSB 149207
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949185	MSB 149208
Canada	Yukon	Lapie River; 8.5 km West of Ross River	KF949186	MSB 149213

Appendix. (cont.)

Country	State/Province	Locality	GenBank	Museum
Canada	Yukon	Campell Hwy (Hwy #4); 3 km N, 7.5 km	KF949187	MSB 149277
Canada	Yukon	Campell Hwy (Hwy #4); 3 km N, 7.5 km	KF949188	MSB 149278
Canada	Yukon	Campell Hwy (Hwy #4); 3 km N, 7.5 km	KF949189	MSB 149280
Canada	Yukon	Campell Hwy (Hwy #4); 3 km N, 7.5 km	KF949190	MSB 149281
Canada	Yukon	45 km East of Dawson on North Klondike	KF949192	MSB 196683
Canada	Yukon	50 km East of Dawson on North Klondike	KF949193	MSB 196689
Canada	Yukon	50 km East of Dawson on North Klondike	KF949194	MSB 196694
Canada	Yukon	35 km S Haines Junction	KF949195	MSB 240548
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949199	MSB 144270
Canada	Yukon	15 mi W Stewart Crossing on Hwy 2	KF949200	MSB 144285
Canada	Yukon	Alaska Highway	KF949205	UAM 35344
Canada	Yukon	Alaska Highway	KF949206	UAM 52704
Canada	Yukon	North Fork of Klondike River on Hwy 5	KF949207	MSB 145251
Canada	Yukon	30 km South of tombstone Territorial Park	KF949267	MSB 196688
Canada	Yukon	Alaska Highway	KF949268	UAM 34604
Canada	Yukon	30 km S of Tombstone Territorial Park	KF964333	MSB 196687
Canada	Yukon	Alaska Highway	EF100721	UAM 52703
		Peromyscus gossypinus		
USA	Arkansas	MN124380	TTU 57149	Jonesboro
USA	Florida	1 mi S, 4.5 mi W Iamonia, Woodyard	DQ385625	MSB 53305
USA	Texas	White Oak Creek WMA	DQ973102	TTU 80682
		Peromyscus leucopus		
Mexico	Tamaulipas	30 km W, 30 km N Soto la Marina	KY064165	TTU 110197
USA	Missouri	5.1 mi NE Armstrong, Westwind Farm	MN124383	TTU 119254
USA	Texas	0.5 mi E Afton	AF131926	TK 47506